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01 10 Intelligenetics
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Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "narrow_spt" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "swope073.key":
narrow_ktxs (AA) ID narrow_ktxs AA preliminary pattern

1 vhtgtsig

Selected files:

File : lacktxs_spt.pep

-- Output Parameters --

Format Options: File Options:
Nucleic acid code matching Exact Indirect file
Find non-matching hits only No Sequence or key file
Report key used Yes List of hits
Note position of hit Yes Hit display
Display full annotations Yes Name and annotations
Sequence context 50 Yes

-- Run Parameters --

Run mode Batch
Time to start comparison now
Notify at end of run No

1 match found in sequence:

024684 ; Bla IAT-3 (Fragment).

(from "lacktxs_spt.pep")

TOIG of: 024684 check: 557 from: 1 to: 381

ID 024684 PRELIMINARY: PRT; 381 AA.
AC 024684;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Bla IAT-3 (Fragment).
GN AMPC.
OS Salmonella seftenberg.
OC Plasmid pSENF.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=28150;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SENF;
RX MEDLINE=97375066; PubMed=9231418;
RA Koeck J.L., Arlet G., Philippin A., Basmaciogullari S., Thien H.V.,
Blissner Y., Cavallo J.D.;
RT "A plasmid-mediated CMY-2 beta-lactamase from an Algerian clinical
isolate of Salmonella seftenberg".
RL FEMS Microbiol. Lett. 152:255-260(1997).
DR HSSP; P00811; 1C3B.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Plasmid.
FT NON_TER 381
SQ SEQUENCE 381 AA; 41973 MW; BE366336B403A87F CRC64;

024684 Length: 381 March 17, 2003 12:32 Type: P Check: 557
Found using 'narrow_ktxs' (swope073.key)

283 GDMYQGLGEMLNWPLKADSIINGSKVALAALPAVEVNPVPAVKASWVHTGSGGP
333 340

343 GSYVAFVPEKNLGIIVMLANKSYNPVVEAAMRIIEKLQ

1 match found in sequence:

032352 ; Beta lactamase class C (Fragment).

(from "lacktxs_spt.pep")

TOIG of: 032352 check: 748 from: 1 to: 381

ID 032352 PRELIMINARY: PRT; 381 AA.
AC 032352;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta lactamase class C (Fragment).
GN BLA CF H224.
OS Citrobacter freundli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H224;
RX MEDLINE=99085658; PubMed=9868767;
RA Verdet C., Arlet G., Ben Redjeb S., Ben Hassan A., Lagrange P.H.,
Philippin A.;
RT "Characterization of CMY-4, an AmpC-type plasmid-mediated beta-
lactamase in a Tunisian clinical isolate of Proteus mirabilis".
RL FEMS Microbiol. Lett. 169:235-240(1998).
DR HSSP; Y15129; CAA75401.1; .
DR HSSP; P00811; 1C3B.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
FT NON_TER 381
SQ SEQUENCE 381 AA; 42013 MW; 7EFBDC93A217D238 CRC64;
032352 Length: 381 March 17, 2003 12:32 Type: P Check: 748
Found using 'narrow_ktxs' (swope073.key)

283 GDMYQGLGEMLNWPLKADSIINGSKVALAALPAVEVNPVPAVKASWVHTGSGGP
333 340

343 GSYVAFVPEKNLGIIVMLANKSYNPVVEAAMRIIEKLQ

1 match found in sequence:

032446 ; Beta-lactamase class C (CEPHAMYCINASE) (Fragment).

(from "lacktxs_spt.pep")

TOIG of: 032446 check: 59 from: 1 to: 381

ID 032446 PRELIMINARY: PRT; 381 AA.
AC 032446;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-lactamase class C (CEPHAMYCINASE) (Fragment).
GN BLA CMY-3 OR CMY-4 OR BLACMY-4.
OS Proteus mirabilis, and
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

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OC Proteus.
OX NCBI_TaxID=584, 562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H223B;
RA Verdet C., Arlet G., Ben Redjeb S., Lagrange P.H., Philippou A.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=22317, AND LAR;
RA Decre D., Raskine L., Blanchard H., Sanson-Le Pors M.J., Petit J.C.,
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=79;
RA Stapleton P.D., Shannon K.P., French G.L.;
RT "Carbapenem resistance in Escherichia coli associated with plasmid-
RT determined CMY-4 beta-lactamase production and loss of an outer
RT membrane protein."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RA Zhao S., White D.G., McDermott P.F., Walker R.D.;
RT "Identification and Expression of Cephamycinase blaCMY Genes in
RT Escherichia coli and Salmonella Isolated from Food Animals and Ground
RT Meats."
RL Antimicrob. Agents Chemother. 0:0-0(2001).
DR EMBL: Y15130; CAA75402.1; -
DR EMBL: Y16783; CAA76380.1; -
DR EMBL: Y16782; CAA76379.1; -
DR EMBL: AF420597; AAL16928.1; -
DR HSSP: P00811; IC3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
FT NON_TER 381
SQ SEQUENCE 381 AA; 41973 MW; CE62C01822AFC416 CRC64;

033446 Length: 381 March 17, 2003 12:32 Type: P Check: 59
Found using 'narrow_ktxs' (swope073.key)

283 GDMYQGLGWEMLNWPLKADSIINGSDSKVALALPAVEVNPAPAVKASWVHKSTGSGF
|-----|
333 340
343 GSYVAFVPEKNIGIVMLANKSYPNPVRVEAMRILEKIQ

1 match found in sequence:
053044 ; Beta-lactamase class C (Fragment).
(from "lactxs_spt.pep")
TOIG of: 053044 check: 59 from: 1 to: 381

ID 053044 PRELIMINARY; PRT; 381 AA.
AC 053044;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-lactamase class C (Fragment).
GN BLA CMY-3.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH 9701;

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RA Decre D., Raskine L., Blanchard H., Sanson-Le Pors M.J., Petit J.C.,
RA Philippou A., Arlet G.;
RT "Importation and characterization of CMY-type beta-lactamases from
RT Proteus mirabilis and Klebsiella pneumoniae in four parisian
RT hospitals."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y16781; CAA76378.1; -
DR HSSP: P00811; IC3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
FT NON_TER 381
SQ SEQUENCE 381 AA; 41973 MW; CE62C01822AFC416 CRC64;

053044 Length: 381 March 17, 2003 12:32 Type: P Check: 59
Found using 'narrow_ktxs' (swope073.key)

283 GDMYQGLGWEMLNWPLKADSIINGSDSKVALALPAVEVNPAPAVKASWVHKSTGSGF
|-----|
333 340
343 GSYVAFVPEKNIGIVMLANKSYPNPVRVEAMRILEKIQ

1 match found in sequence:
054038 ; Beta-lactamase class C (Fragment).
(from "lactxs_spt.pep")
TOIG of: 054038 check: 980 from: 1 to: 381

ID 054038 PRELIMINARY; PRT; 381 AA.
AC 054038;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-lactamase class C (Fragment).
GN BLA CMY-4.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=34955;
RA Decre D., Raskine L., Blanchard H., Sanson-Le Pors M.J., Petit J.C.,
RA Philippou A., Arlet G.;
RT "Importation and characterization of CMY-type beta-lactamases from
RT Proteus mirabilis and Klebsiella pneumoniae in four parisian
RT hospitals."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y16785; CAA76382.1; -
DR HSSP: P00811; IC3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
FT NON_TER 381
SQ SEQUENCE 381 AA; 42016 MW; 6323F9ECCTC3A1A CRC64;

054038 Length: 381 March 17, 2003 12:32 Type: P Check: 980
Found using 'narrow_ktxs' (swope073.key)

283 GDMYQGLGWEMLNWPLKADSIINGSDSKVALALPAVEVNPAPAVKASWVHKSTGSGF
|-----|
333 340
343 GSYVAFVPEKNIGIVMLANKSYPNPVRVEAMRILEKIQ

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1 match found in sequence:
069409 ; Ampc-type beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: 069409 check: 744 from: 1 to: 381

ID 069409 PRELIMINARY; PRT; 381 AA.
AC 069409;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Ampc-type beta-lactamase.
OS Enterobacteriaceae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=550;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98377722; PubMed=9711843;
RA Morosini M.I., Negri M.C., Sholchet B., Baquero M.R., Baquero F.,
Blazquez J.;
RT "An extended-spectrum Ampc-type beta-lactamase obtained by in vitro
antibiotic selection.";
RL FEMS Microbiol. Lett. 165:85-90(1998).
DR EMBL; AJ005633; CAA06639.1; -.
DR HSSP; P05364; 2BLF.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 41301 MW; 49D127F268B75C3C CRC64;

069409 Length: 381 March 17, 2003 12:32 Type: P Check: 744 ..
Found using 'narrow_ktxs' (swope073.key)

283 GSWYQGLGEMINMPVEANTVEGSDSKVALALPPEAEVNPAPPYKASWVHKGTSTGCF
333 340

343 GSYVAFPEKNGIYMLANKSYNPAPVAYHILEALQ

1 match found in sequence:
q46038 ; Beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q46038 check: 450 from: 1 to: 381

ID 046038 PRELIMINARY; PRT; 381 AA.
AC 046038;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Beta-lactamase.
GN AMPC.
OS Citrobacter freundli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1113;
RA Bennett P.M., Damdinsuren E., Jones M.E.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X76636; CAA54084.1; -.
DR HSSP; P00811; 1C3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 42109 MW; E7DE776F2419B34 CRC64;

046038 Length: 381 March 17, 2003 12:32 Type: P Check: 450 ..

Found using 'narrow_ktxs' (swope073.key)

283 GEMVQGLGEMINMPKADIVINSKIALALPAVEVNPAPVYKASWVHKGTSTGCF
333 340

343 GSYVAFPEKNGIYMLANKSYNPAPVAYHILEALQ

1 match found in sequence:
q46041 ; Beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q46041 check: 1146 from: 1 to: 381

ID 046041 PRELIMINARY; PRT; 381 AA.
AC 046041;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Beta-lactamase.
OS Citrobacter freundli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GC3;
RA Haruta S., Taniguchi K., Nukaga M., Sawai T.;
RT "The nucleotide sequence and characterization of the extended-spectrum
class C beta-lactamase from Citrobacter freundli GC3.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D85910; BA012916.1; -.
DR HSSP; P00811; 1C3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 41841 MW; 5D70308A5C7FD370 CRC64;

046041 Length: 381 March 17, 2003 12:32 Type: P Check: 1146 ..
Found using 'narrow_ktxs' (swope073.key)

283 GDMVQGLGEMINMPKADISITNGSDSKVALALPAVEVNPAPVYKASWVHKGTSTGCF
333 340

343 GSYVAFPEKNGIYMLANKSYNPAPVAYHILEALQ

1 match found in sequence:
q48428 ; Beta-lactamase ACT-1.
(from "lactxs_spt.pep")
TOIG of: q48428 check: 4454 from: 1 to: 381

ID 048428 PRELIMINARY; PRT; 381 AA.
AC 048428;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Beta-lactamase ACT-1.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MCO-95;
RX MEDLINE=97209051; PubMed=9055993;
RX Bradford P.A., Urban C., Mariano N., Projan S.J., Rahal J.J., Bush K.;

RT "Imipenem resistance in Klebsiella pneumoniae is associated with the
 RT combination of ACT-1, a plasmid-mediated AmpC beta-lactamase, and the
 RT foci of an outer membrane protein."
 RL Antimicrob. Agents Chemother. 41:563-569(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MC-95;
 RA Bradford P.A., Urban C., Mariano N., Rahal J., Bush K.;
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U58495; AAC45086.2; -.
 DR HSSP: P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase_1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 381 AA; 41572 MW; 3A5038DDA7DE3878 CRC64;
 Q48428 Length: 381 March 17, 2003 12:32 Type: P Check: 4454 ..
 Found using 'narrow_ktxs' (swope073.key)
 ...
 284 GATGGLGEMLMNPVDAKTVESGDNKVALAPLPAREVNPAPPVNASWYHKTGSTGCF
 334 341
 344 GSYVAFPEKNGIWMANKSYNPVREAVARILSLAL

 1 match found in sequence:
 q48433; EXTENDED SPECTRUM beta-lactamase precursor.
 (from "lactxs_spt.pep")
 TOIG of: q48433 check: 309 from: 1 to: 381
 ID Q48434 PRELIMINARY; PRT; 381 AA.
 AC Q48434;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE EXTENDED SPECTRUM beta-lactamase precursor.
 GN BIA CMY-2.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Hel-1;
 RA MEDLINE-96379697; PubMed-8787910;
 RA Bauerfeld A., Stemplinger J., Jungwirth R., Giamarelion H.;
 RT "Characterization of the plasmidic beta-lactamase CMY-2, which is
 RT responsible for cephamycin resistance."
 RL Antimicrob. Agents Chemother. 40:221-224(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=169;
 RA Decre D., Raakine L., Blancard H., Sanson-Le Pors M.J., Petit J.C.,
 RA Philippou A., Aillet G.;
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: X91840; CA62957.1; -.
 DR EMBL: Y16784; CA676381.1; -.
 DR HSSP: P00811; 1C3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase_1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 381
 SQ SEQUENCE 381 AA; 42003 MW; 8C30E62E52DFC311 CRC64;
 Q48434 Length: 381 March 17, 2003 12:32 Type: P Check: 309 ..
 Found using 'narrow_ktxs' (swope073.key)

...
 283 GDMYGLGEMLMNPDKADSIINGSDSKVALAALPAVEVNPAPPAKASWYHKTGSTGCF
 333 340
 343 GSYVAFPEKNGIWMANKSYNPVREAVARILEKLO

 1 match found in sequence:
 q48433; LAT-2 B-lactamase precursor.
 (from "lactxs_spt.pep")
 TOIG of: q48433 check: 9885 from: 1 to: 381
 ID Q48435 PRELIMINARY; PRT; 381 AA.
 AC Q48435; 008034; (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE LAT-2 B-lactamase precursor.
 GN BIA LAT-2.
 OS Klebsiella pneumoniae.
 OC Plasmid pMEL.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WILD N5.
 RA Gazouli M., Tzouveleletis L.S., Primarakis E., Miriagou V., Tzelepi E.;
 RT "Transferable cefoxitin resistance in enterobacteria from Greek
 RT hospitals and characterization of a plasmid-mediated group 1 beta-
 RT lactamase (LAT-2)."
 RL Antimicrob. Agents Chemother. 40:1736-1740(1996).
 DR EMBL: X97039; CA65752.1; -.
 DR EMBL: S83226; ABA6884.1; -.
 DR HSSP: P00811; 1C3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase_1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Plasmid; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 381
 SQ SEQUENCE 381 AA; 42036 MW; ED951747D7597B6A CRC64;
 Q48435 Length: 381 March 17, 2003 12:32 Type: P Check: 9885 ..
 Found using 'narrow_ktxs' (swope073.key)
 ...
 283 GDMYGLGEMLMNPDKADSIINGSDSKVALAALPAVEVNPAPPAKASWYHKTGSTGCF
 333 340
 343 GSYVAFPEKNGIWMANKSYNPVREAVARILEKLO

 1 match found in sequence:
 q48433; Beta-lactamase precursor.
 (from "lactxs_spt.pep")
 TOIG of: q48433 check: 488 from: 1 to: 381
 ID Q48443 PRELIMINARY; PRT; 381 AA.
 AC Q48443;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)


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DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Beta-lactamase precursor.
GN BLATAT-1.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
NCBI_TaxID=573;
OX
RN
RP SEQUENCE FROM N.A.
RC STRAIN=WILD STRAIN P20;
RX MEDLINE=95110098; PubMed=7811049;
RA Tzouvelekis L.S., Tzelepi E., Mentis A.F.;
RT "Nucleotide sequence of a plasmidic cephalosporinase gene (bla-LAT-1)
found in Klebsiella pneumoniae."
RL Antimicrob. Agents Chemother. 38:2207-2209(1994).
DR EMBL: X78117; CAAS5007.1; -.
DR HSSP: P00811; IC3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW Signal.
FT SIGNAL. 1 20 POTENTIAL.
FT CHAIN 21 381 MATURE BETA-LACTAMASE.
SQ SEQUENCE 381 AA; 42047 MW; DEF1356A336E90 CRC64;

Q48443 Length: 381 March 17, 2003 12:32 Type: P Check: 488
Found using 'narrow_ktxs' (swope073.key)

...

283 GDMYGLGWMELNMPKADSIINGSDSKVALALPAVEVNPAPPAVKASVWHTGSGGF
|-----|
333 340

343 GSYAFAVPEKNLGIIVANKSYNPVREAVRLEKIQ

1 match found in sequence:
q59276; Beta-lactamase precursor (EC 3.5.2.6).
(from "lactxs_spt.pep")
TOIG of: q59276 check: 730 from: 1 to: 381

ID 059276 PRELIMINARY; PRT; 381 AA.
AC 059276;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
RT "Role of lysine-67 in the active site of class C beta-lactamase from
Citrrobacter freundii GN346."
RL Eur. J. Biochem. 188:15-22(1990).
DR EMBL: D13207; BAA02494.1; -.
DR HSSP: P00811; IC3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.

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DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW Hydrolase; Signal. 20 POTENTIAL.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 381 BETA-LACTAMASE.
SQ SEQUENCE 381 AA; 42013 MW; E949AC92F314F338 CRC64;

Q59276 Length: 381 March 17, 2003 12:32 Type: P Check: 720
Found using 'narrow_ktxs' (swope073.key)

...

283 GDMYGLGWMELNMPKADSIINGSDSKVALALPAVEVNPAPPAVKASVWHTGSGGF
|-----|
333 340

343 GSYAFAVPEKNLGIIVANKSYNPVREAVRLEKIQ

1 match found in sequence:
q59401; Class C beta-lactamase precursor (EC 3.5.2.6).
(from "lactxs_spt.pep")
TOIG of: q59401 check: 2391 from: 1 to: 384

ID 059401 PRELIMINARY; PRT; 384 AA.
AC 059401;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
RT "Cloning and sequence analysis of blaBil-1, a plasmid-mediated class C
beta-lactamase gene in Escherichia coli BS."
RL Antimicrob. Agents Chemother. 38:1182-1185(1994).
DR EMBL: X74512; CAAS2618.1; -.
DR HSSP: P00811; IC3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW Hydrolase.
SQ SEQUENCE 381 AA; 42084 MW; C8125021E195CC1 CRC64;

Q59398 Length: 381 March 17, 2003 12:32 Type: P Check: 861
Found using 'narrow_ktxs' (swope073.key)

...

283 GDMYGLGWMELNMPKADSIINGSDTKVALAALPAVEVNPAPPAVKASVWHTGSGGF
|-----|
333 340

343 GSYAFAVPEKNLGIIVANKSYNPVREAVRLEKIQ

1 match found in sequence:
q59398; Beta-lactamase (EC 3.5.2.6).
(from "lactxs_spt.pep")
TOIG of: q59398 check: 861 from: 1 to: 381

ID 059398 PRELIMINARY; PRT; 381 AA.
AC 059398;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Beta-lactamase (EC 3.5.2.6).
GN BLA Bil-1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
NCBI_TaxID=562;
OX
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BS;
RX MEDLINE=94346831; PubMed=8067761;
RA Fosperry AP., Payne D.J., Lawlor E.J., Hodgson J.E.;
RT "Cloning and sequence analysis of blaBil-1, a plasmid-mediated class C
beta-lactamase gene in Escherichia coli BS."
RL Antimicrob. Agents Chemother. 38:1182-1185(1994).
DR EMBL: X74512; CAAS2618.1; -.
DR HSSP: P00811; IC3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW Hydrolase.
SQ SEQUENCE 381 AA; 42084 MW; C8125021E195CC1 CRC64;

```

DE Class C beta-lactamase precursor (EC 3.5.2.6).
 OS Enterobacteriaceae;
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter;
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GC1;
 RX MEDLINE=95197591; PubMed=7890700;
 RA Nukaga M., Haruta S., Tanimoto K., Kogure K., Taniguchi K., Tamaki M.,
 RA Sawai T.;
 RT "Molecular evolution of a class C beta-lactamase extending its
 RT substrate specificity.";
 RT J. Biol. Chem. 270:5729-5735(1995).
 DR EMBL: D44479; BAA07922.1; -;
 DR HSSP: P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase_1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 384 CLASS C BETA-LACTAMASE.
 SQ SEQUENCE 384 AA: 41612 MW: B3BC13B0251372P CRC64;
 Q59401 Length: 384 March 17, 2003 12:32 Type: P Check: 2391 ..
 Found using 'narrow_ktxs' (swope073.key)

346 GSYVAFPEKQIGIVMLANTSYNPAPVPAVAKASVWHTGSTGCF
 286 GSYVAFPEKQIGIVMLANTSYNPAPVPAVAKASVWHTGSTGCF
 336 343

1 match found in sequence:
 q8rml0 : AmpC.
 (from "lacktxs_spt.pep")
 TOIG of: q8rml0 check: 218 from: 1 to: 381

ID 08RML0 PRELIMINARY; PRT; 381 AA.
 AC 08RML0.
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE AmpC.
 GN AMPC.
 OS Citrobacter werkmanii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Citrobacter.
 OX NCBI_TaxID=67827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Naas T., Aubert D., Fortineau N., Nordmann P.;
 RT "Cloning and sequencing of five genes encoding AmpC beta-lactamase and
 RT their regulator genes from Citrobacter braakii, Citrobacter murliniae,
 RT Citrobacter werkmanii, Escherichia fergusonii and Enterobacter
 RT cancerogenus.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF492448; AAM11670.1; -;
 SQ SEQUENCE 381 AA: 41978 MW: FE5E048364849857 CRC64;
 Q8RML0 Length: 381 March 17, 2003 12:32 Type: P Check: 218 ..
 Found using 'narrow_ktxs' (swope073.key)

283 GDMYGLGEMLMNPVNAADSIINGSDSKVALALPAVEVNPAPPAVAKASVWHTGSTGCF
 333 340

343 GSYVAFPEKQIGIVMLANKSYNPAPVPAVAKASVWHTGSTGCF
 283 GDMYGLGEMLMNPVNAADSIINGSDSKVALALPAVEVNPAPPAVAKASVWHTGSTGCF
 333 340

1 match found in sequence:
 q8rml2 : AmpC.
 (from "lacktxs_spt.pep")
 TOIG of: q8rml2 check: 1086 from: 1 to: 381

ID 08RML2 PRELIMINARY; PRT; 381 AA.
 AC 08RML2.
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE AmpC.
 GN AMPC.
 OS Citrobacter braakii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Citrobacter.
 OX NCBI_TaxID=57706;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Naas T., Aubert D., Fortineau N., Nordmann P.;
 RT "Cloning and sequencing of five genes encoding AmpC beta-lactamase and
 RT their regulator genes from Citrobacter braakii, Citrobacter murliniae,
 RT Citrobacter werkmanii, Escherichia fergusonii and Enterobacter
 RT cancerogenus.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF492447; AAM11668.1; -;
 SQ SEQUENCE 381 AA: 41929 MW: C72115D6462B3CF CRC64;
 Q8RML2 Length: 381 March 17, 2003 12:32 Type: P Check: 1086 ..
 Found using 'narrow_ktxs' (swope073.key)

343 GSYVAFPEKQIGIVMLANKSYNPAPVPAVAKASVWHTGSTGCF
 283 GDMYGLGEMLMNPVNAADSIINGSDSKVALALPAVEVNPAPPAVAKASVWHTGSTGCF
 333 340

1 match found in sequence:
 q8rml4 : AmpC.
 (from "lacktxs_spt.pep")
 TOIG of: q8rml4 check: 4995 from: 1 to: 381

ID 08RML4 PRELIMINARY; PRT; 381 AA.
 AC 08RML4.
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE AmpC.
 GN AMPC.
 OS Enterobacter cancerogenus.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=69218;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Naas T., Aubert D., Fortineau N., Nordmann P.;
 RT "Cloning and sequencing of five genes encoding AmpC beta-lactamase and
 RT their regulator genes from Citrobacter braakii, Citrobacter murliniae,
 RT Citrobacter werkmanii, Escherichia fergusonii and Enterobacter
 RT cancerogenus.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF492446; AAM11666.1; -;
 SQ SEQUENCE 381 AA: 41357 MW: ACB32217AEDAC11C CRC64;
 Q8RML4 Length: 381 March 17, 2003 12:32 Type: P Check: 4995 ..
 Found using 'narrow_ktxs' (swope073.key)

283

GSMTGGLGEMLNMPVDKTIIDSDNKIALALPAREVNPAPPVKASWVHKSTGTF
333 340

343

GSYVAFIPEKQIGIVMLANKSYNPAPVAYOILNALQ

1 match found in sequence:

q8rm16 : AmpC.
(from "lactixs_spt.pep")
TOIG of: q8rm16 check: 711 from: 1 to: 381

ID

Q8RML6 PRELIMINARY; PRT; 381 AA.

AC

Q8RML6; 01-JUN-2002 (TREMBlrel. 21, Created)

DT

01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT

01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE

AmpC.

GN

AmpC.

OS

Citrobacter murlinae.

OC

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OT

Citrobacter.

OX

NCBI_TaxID=67829;

RN

[1]

RP

SEQUENCE FROM N.A.

RA

Naas T., Albert D., Fortinneau N., Nordmann P.;

RT

"Cloning and sequencing of five genes encoding AmpC beta-lactamase and their regulator genes from Citrobacter braakii, Citrobacter murlinae,

RT

Citrobacter werkmanii, Escherichia fergusonii and Enterobacter

RT

cancerogenus.";

RL

Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR

EMBL; AF492445; AA011664.1; C8CE1A21711DF765 CRC64;

SQ

SEQUENCE 381 AA; 42107 MW; C8CE1A21711DF765 CRC64;

...

283

GEMTGLGEMLNMPVKADIVINGSKIALALPAVEVNPAPPVKASWVHKSTGTF
333 340

343

GSYVAFIPEKQIGIVMLANKSYNPAPVADAMRILEKLO

1 match found in sequence:

q8vk20 : Beta-lactamase (Fragment).
(from "lactixs_spt.pep")
TOIG of: q8vk20 check: 7371 from: 1 to: 372

ID

Q8VKZ0 PRELIMINARY; PRT; 372 AA.

AC

Q8VKZ0; 01-MAR-2002 (TREMBlrel. 20, Created)

DT

01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT

01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE

Beta-lactamase (Fragment).

GN

AmpC.

OS

Enterobacter dissolvens.

OC

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OT

Enterobacter.

OX

NCBI_TaxID=69219;

RN

[1]

RP

SEQUENCE FROM N.A.

RA

Rotman M.M., Benzerara L., Hanau B., Arlet G.;

RT

"Variability of the ampC gene among species belonging to genus

RT

Enterobacter.";

RL

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR

EMBL; AJ311363; CAC85359.1; -

DR

InterPro; IPR001466; Beta_lactamase.

OS

InterPro; IPR001586; Beta_lactamase_C.

DR Pfam; PF00144; beta-lactamase; 1.

DR PROSITE; PS00336; BETA_LACTAMASE_C; UNKNOWN_1.

FT NON_TER 1 1

FT NON_TER 372 372

SQ SEQUENCE 372 AA; 40386 MW; 34209577B608C3A CRC64;

Q8VKZ0 Length: 372 March 17, 2003 12:32 Type: P Check: 7371 ..

Found using 'narrow_ktxs' (swope073.key)

...

282

GAMTGLGEMLNMPVDKTVVDSGDNKVALALPAPAEVNPAPPVKASWVHKSTGTF
332 339

342

GSYVAFIPEKQIGIVMLANKSYNPAPVAVETA

1 match found in sequence:

q8vk21 : Beta-lactamase.
(from "lactixs_spt.pep")
TOIG of: q8vk21 check: 8607 from: 1 to: 381

ID

Q8VKZ1 PRELIMINARY; PRT; 381 AA.

AC

Q8VKZ1; 01-MAR-2002 (TREMBlrel. 20, Created)

DT

01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT

01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE

Beta-lactamase.

GN

AmpC.

OS

Enterobacter hormaechei.

OC

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OT

Enterobacter.

OX

NCBI_TaxID=158836;

RN

[1]

RP

SEQUENCE FROM N.A.

RC

STRAIN-CIP 103441T;

RA

Rotman M.M., Benzerara L., Hanau B., Arlet G.;

RT

"Variability of the ampC gene among species belonging to genus

RT

Enterobacter.";

RL

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR

EMBL; AJ311364; CAC85357.1; -

DR

InterPro; IPR001466; Beta_lactamase.

DR

InterPro; IPR001586; Beta_lactamase_C.

DR

Pfam; PF00144; beta-lactamase; 1.

SQ

PROSITE; PS00336; BETA_LACTAMASE_C; UNKNOWN_1.

SQ

SEQUENCE 381 AA; 41444 MW; 3852D04B9F237BA0 CRC64;

...

283

GSMTGGLGEMLNMPVKAFTVIEGSDNKVALALPAPAEVNPAPPVKASWVHKSTGTF
333 340

343

GSYVAFIPEKQIGIVMLANKSYNPAPVAYHILDALQ

1 match found in sequence:

q8vk22 : AmpC beta-lactamase.
(from "lactixs_spt.pep")
TOIG of: q8vk22 check: 2566 from: 1 to: 381

ID

Q8VKZ2 PRELIMINARY; PRT; 381 AA.

AC

Q8VKZ2; 01-MAR-2002 (TREMBlrel. 20, Created)

DT

01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT

01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE

AmpC beta-lactamase.

GN

AmpC.

OS

Enterobacter asburiae.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=61645;
 RN [1]
 RC STRAIN=CIP 103358 T;
 RA Rottman M.M.;
 RL Thesis (2001), Faculte de Medecine Necker-Enfants malades, Paris, France.
 DR EMBL: AJ311172; CAC85157.1;
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase.C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.
 SQ SEQUENCE 381 AA; 41481 MW; 37205666681D71 CRC64;
 O8VKZ2 Length: 381 March 17, 2003 12:32 Type: P Check: 2566 ..
 Found using 'narrow_ktxs' (swope073.key)

283 GMYOGLGEMLNMPVDKTVESGDNKVALAPLPAREVNPAPVPKASVWYHKTGSTGCF
 333 340
 343 GSYVAFIPEKQGIWMLANKSYNPAPVEMAYRILSALQ

1 match found in sequence:
 q8vnm2 : Beta_lactamase (Fragment).
 (from "lactxs_spt.pep")
 TOIG of: q8vnm2 check: 4483 from: 1 to: 381

ID Q8VNM2 PRELIMINARY; PRT; 381 AA.
 AC Q8VNM2;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Beta_lactamase (Fragment).
 GN AMPC.
 OS Enterobacter intermedius.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=61648;
 RN [1]
 RC STRAIN=CIP 79.27T(ATCC 33110);
 RA Rottman M.M., Benzerrara L., Hanau B., Arlet G.;
 RL "Variability of the ampc gene among species belonging to genus Enterobacter";
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ311365; CAC85358.1;
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase.C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.
 FT NON_TER 1 1
 FT NON_TER 381 381
 SQ SEQUENCE 381 AA; 41298 MW; 0DE390FB6759C792 CRC64;

O8VNM2 Length: 381 March 17, 2003 12:32 Type: P Check: 4483 ..
 Found using 'narrow_ktxs' (swope073.key)

282 GMYOGLGEMLNMPVDKTVGSDNKVALALPYKEVNPAPVPKASVWYHKTGSTGCF
 332 339
 342 GSYVAFIPEKQGIWMLANKSYNPAPVEMAYRILSALQ
 1 match found in sequence:

q8vnt7 : Beta-lactamase (Fragment).
 (from "lactxs_spt.pep")
 TOIG of: q8vnt7 check: 3072 from: 1 to: 373
 O8VNT7 Length: 373 March 17, 2003 12:32 Type: P Check: 3072 ..
 Found using 'narrow_ktxs' (swope073.key)

283 GMYOGLGEMLNMPVDKTTIDSGDNKIALALPAREVNPAPVPKASVWYHKTGSTGCF
 333 340

343 GSYVAFIPEKQGIWMLANKSYNPAPVEMAYRILSALQ

1 match found in sequence:
 q933m6 : Beta-lactamase AmpC precursor (EC 3.5.2.6).
 (from "lactxs_spt.pep")
 TOIG of: q933m6 check: 1351 from: 1 to: 381

ID Q933M6 PRELIMINARY; PRT; 381 AA.
 AC Q933M6;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Beta-lactamase AmpC precursor (EC 3.5.2.6).
 GN AMPC.
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RC STRAIN=K99230, K9911729, AND K9914325;
 RA Lee S.H., Jeong S.H., Lee K.J.;
 RL "Complete sequence of AmpC beta-lactamase gene";
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF411146; AAL05855.1;
 DR EMBL: AF411147; AAL05856.1;
 DR EMBL: AF411149; AAL05858.1;
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase.C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.
 KW Hydrolase; Signal.

FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 381 BETA-LACTAMASE AMPC.
 SQ SEQUENCE 381 AA; 41251 MW; 67912CB5C8D3C93 CRC64;
 Q933M6 Length: 381 March 17, 2003 12:32 Type: P Check: 1351 ..
 Found using 'narrow_ktxs' (swope073.key)

283 GSNYGLGEMLMNPVEANTVVEGSDSKVALAPLPAVEVNPAPPVKASWVHKGTSTGCF
 333 340

343 GSYVAFIPEKQIGIVMLANKSYNPAPVAAVHILEALQ

1 match found in sequence:
 q933r1 : Beta-lactamase AmpC precursor (EC 3.5.2.6).
 (from "lactxs_spt.pep")
 TOIG of: q933r1 check: 1305 from: 1 to: 381

ID Q933R1 PRELIMINARY; PRT; 381 AA.
 AC Q933R1;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Beta-lactamase AmpC precursor (EC 3.5.2.6).
 GN AMPC.
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=530;
 [1]
 RN SEQUENCE FROM N.A.
 RC SPRAIN-K992004.1, AND K995120.1;
 RA Lee S.H., Jeong S.H., Lee K.J.;
 RT "Complete sequence of AmpC beta-lactamase gene";
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF411144; AAL05853.1; -
 DR EMBL; AF411145; AAL05854.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 381 BETA-LACTAMASE AMPC.
 SQ SEQUENCE 381 AA; 41271 MW; 50013E3B8B875C2F CRC64;
 Q933R1 Length: 381 March 17, 2003 12:32 Type: P Check: 1305 ..
 Found using 'narrow_ktxs' (swope073.key)

283 GSNYGLGEMLMNPVEANTVVEGSDSKVALAPLPAVEVNPAPPVKASWVHKGTSTGCF
 333 340

343 GSYVAFIPEKQIGIVMLANKSYNPAPVAAVHILEALQ

1 match found in sequence:
 q93ca2 : Beta-lactamase AmpC precursor (EC 3.5.2.6).
 (from "lactxs_spt.pep")
 TOIG of: q93ca2 check: 2682 from: 1 to: 381

ID Q93CA2 PRELIMINARY; PRT; 381 AA.
 AC Q93CA2;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Beta-lactamase AmpC precursor (EC 3.5.2.6).
 GN AMPC.

OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=530;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K9973;
 RA Lee S.H., Jeong S.H., Lee K.J.;
 RT "Complete sequence of AmpC beta-lactamase gene";
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF411148; AAL05857.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 381 BETA-LACTAMASE AMPC.
 SQ SEQUENCE 381 AA; 41341 MW; 31A3C4659A361921 CRC64;

Q93CA2 Length: 381 March 17, 2003 12:32 Type: P Check: 2682 ..
 Found using 'narrow_ktxs' (swope073.key)

283 GSNYGLGEMLMNPVEANTVVEGSDSKVALAPLPAVEVNPAPPVKASWVHKGTSTGCF
 333 340

343 GSYVAFIPEKQIGIVMLANTSYNPAPVAAVHILEALQ

1 match found in sequence:
 q9afg7 : Class C beta-lactamase.
 (from "lactxs_spt.pep")
 TOIG of: q9afg7 check: 9615 from: 1 to: 381

ID Q9AFG7 PRELIMINARY; PRT; 381 AA.
 AC Q9AFG7;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Class C beta-lactamase.
 GN AMPC.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Citrobacter.
 OX NCBI_TaxID=546;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-ATCC:6454;
 RA Barlow M., Hall B.G.;
 RT "Origin and Evolution of the ampc b-lactamases of Citrobacter
 freundii";
 RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF349570; AAK32688.1; -
 DR HSRP: P00811; IC3B
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 381 AA; 41948 MW; B5AC0DBB81FD0742 CRC64;

Q9AFG7 Length: 381 March 17, 2003 12:32 Type: P Check: 9615 ..
 Found using 'narrow_ktxs' (swope073.key)

283 GSNYGLGEMLMNPVLAADSIINGSDSKVALAPLPAVEVNPAPPVKASWVHKGTSTGCF
 333 340

343 GSYVAFVEPEKNLIGIVMLANKSYNPAPVAAVHILEALQ

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1 match found in sequence:
q9f498 : Class C beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q9f498 check: 668 from: 1 to: 381

ID Q9AFG8 PRELIMINARY; PRT; 381 AA.
AC Q9AFG8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Class C beta-lactamase.
GN Ampc.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_Taxid=546;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC:6879;
RA Barlow M., Hall B.G.;
RT "Origin and Evolution of the ampc b-lactamases of Citrobacter
RT freundii.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349569; AAK32687.1; -.
DR HSSP; P00811; 1C3B.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 42057 MW; 626D564722059D18 CRC64;

Q9AFG8 length: 381 March 17, 2003 12:32 Type: P Check: 668
Found using 'narrow_ktxs' (swope073.key)

...

283 GDMYGLGEMLMNPVPEANTVIEGSDSKVALAPVAVENPPAPVAKASWVHKGTSGF
|-----|
333 340

343 GSYVAFPEKQIGIVMLANKSYNPVAVAEAMRIEKLQ

-----
1 match found in sequence:
q9f491 : Class C beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q9f491 check: 134 from: 1 to: 381

ID Q9F491 PRELIMINARY; PRT; 381 AA.
AC Q9F491;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Class C beta-lactamase.
GN Ampc.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_Taxid=550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ODDHP;
RX MEDLINE=21100285; Pubmed=11179650;
RA Barnaud G., Labia R., Raskine L., Sanson-Le Fors M., Philippou A.,
RA Arlet G.;
RT "Extension of resistance to cefepime and ceftioime associated to a six
RT amino acid deletion in the H-10 helix of the cephalosporinase of an
RT Enterobacter cloacae clinical isolate.";
RL FEMS Microbiol. Lett. 195:185-190(2001).
DR EMBL; AJ278995; CAC08446.1; -.
DR HSSP; P05364; 2BLT.
SQ SEQUENCE 381 AA; 42057 MW; 626D564722059D18 CRC64;

Q9F491 length: 381 March 17, 2003 12:32 Type: P Check: 668
Found using 'narrow_ktxs' (swope073.key)

...

283 GDMYGLGEMLMNPVPEANTVIEGSDSKVALAPVAVENPPAPVAKASWVHKGTSGF
|-----|
333 340

343 GSYVAFPEKQIGIVMLANKSYNPVAVAEAMRIEKLQ

-----
1 match found in sequence:
q9f493 : Class C beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q9f493 check: 6296 from: 1 to: 375

ID Q9F493 PRELIMINARY; PRT; 375 AA.
AC Q9F493;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Class C beta-lactamase.
GN Ampc.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_Taxid=550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHE;
RX MEDLINE=21100285; Pubmed=11179650;
RA Barnaud G., Labia R., Raskine L., Sanson-Le Fors M., Philippou A.,
RA Arlet G.;
RT "Extension of resistance to cefepime and ceftioime associated to a six
RT amino acid deletion in the H-10 helix of the cephalosporinase of an
RT Enterobacter cloacae clinical isolate.";
RL FEMS Microbiol. Lett. 195:185-190(2001).
DR EMBL; AJ278994; CAC08444.1; -.
DR HSSP; P05364; 2BLT.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 375 AA; 40744 MW; B62038B64A128B76 CRC64;

Q9F493 length: 375 March 17, 2003 12:32 Type: P Check: 6296
Found using 'narrow_ktxs' (swope073.key)

...

277 SRVWRIGSMYGLGEMLMNPVPEANTVIEGSDPLVPEVNPAPVAKASWVHKGTSGF
|-----|
327 334

337 GSYVAFPEKQIGIVMLANTSYNPVAVAEAMRIEKLQ

-----
1 match found in sequence:
q9f495 : Beta-lactamase Ampc.
(from "lactxs_spt.pep")
TOIG of: q9f495 check: 1524 from: 1 to: 381

ID Q9F495 PRELIMINARY; PRT; 381 AA.
AC Q9F495;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

```

```

DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 41271 MW; CA9AF09300CDEA9C CRC64;

Q9F491 length: 381 March 17, 2003 12:32 Type: P Check: 134
Found using 'narrow_ktxs' (swope073.key)

...

283 GDMYGLGEMLMNPVPEANTVIEGSDSKVALAPVAVENPPAPVAKASWVHKGTSGF
|-----|
333 340

343 GSYVAFPEKQIGIVMLANKSYNPVAVAEAMRIEKLQ

-----
1 match found in sequence:
q9f493 : Class C beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q9f493 check: 6296 from: 1 to: 375

ID Q9F493 PRELIMINARY; PRT; 375 AA.
AC Q9F493;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Class C beta-lactamase.
GN Ampc.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_Taxid=550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHE;
RX MEDLINE=21100285; Pubmed=11179650;
RA Barnaud G., Labia R., Raskine L., Sanson-Le Fors M., Philippou A.,
RA Arlet G.;
RT "Extension of resistance to cefepime and ceftioime associated to a six
RT amino acid deletion in the H-10 helix of the cephalosporinase of an
RT Enterobacter cloacae clinical isolate.";
RL FEMS Microbiol. Lett. 195:185-190(2001).
DR EMBL; AJ278994; CAC08444.1; -.
DR HSSP; P05364; 2BLT.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 375 AA; 40744 MW; B62038B64A128B76 CRC64;

Q9F493 length: 375 March 17, 2003 12:32 Type: P Check: 6296
Found using 'narrow_ktxs' (swope073.key)

...

277 SRVWRIGSMYGLGEMLMNPVPEANTVIEGSDPLVPEVNPAPVAKASWVHKGTSGF
|-----|
327 334

337 GSYVAFPEKQIGIVMLANTSYNPVAVAEAMRIEKLQ

-----
1 match found in sequence:
q9f495 : Beta-lactamase Ampc.
(from "lactxs_spt.pep")
TOIG of: q9f495 check: 1524 from: 1 to: 381

ID Q9F495 PRELIMINARY; PRT; 381 AA.
AC Q9F495;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

```

```

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Beta-lactamase AmpC.
GN AmpC.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20493130; PubMed=11036041;
RA Preston K.E., Radomski C.C.A., Venezia R.A.;
RT "Nucleotide Sequence of the Chromosomal ampC Gene of Enterobacter
aerogenes."
RL Antimicrob. Agents Chemother. 44:3158-3162(2000).
DR EMBL; AF211348; AAF18992.1; -.
DR HSSP; P05364; 2BLT.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 41601 MW; FA7BF5B8B206C80 CRC64;

Q9RER5 Length: 381 March 17, 2003 12:33 Type: P Check: 1524 ..
Found using 'narrow_ktxs' (swope073.key)

-----1
283 GEMYGGLGEMLMNPVPAEVINGSDNKVALAALPAVEVNPAPPAVKASVWHTGSGTGF
333 340
343 GSYVAFIPQDGLIVMLANKSYNPVERVKAAMRILEKIQ

-----1
1 match found in sequence:
q9s6r4 ; Beta-lactamase (EC 3.5.2.6).
(from "lactxs_spt.pep")
TOIG of: q9s6r4 check: 345 from: 1 to: 381

ID Q9S6R4 PRELIMINARY; PRT; 381 AA.
AC Q9S6R4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Beta-lactamase (EC 3.5.2.6).
GN CMY-7.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMC 27;
RT "Three class C plasmid-mediated beta-lactamases from clinical isolates
of E. coli from Punjab, India."
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RU EMBL; AJ011291; CAB36900.1; -.
DR HSSP; P00811; 1C3B.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Hydrolase.
SQ SEQUENCE 381 AA; 42061 MW; 8B5F5AF82C707FC5 CRC64;

Q9S6R4 Length: 381 March 17, 2003 12:33 Type: P Check: 345 ..
Found using 'narrow_ktxs' (swope073.key)

-----1
283 GDMYQGLGEMLMNPPLKADSIINGSDSKVALAALPAVEVNPAPPAVKASVWHTGSGTGF
333 340
343 GSYVAFIPQDGLIVMLANKSYNPVERVKAAMRILEKIQ

-----1
1 match found in sequence:
q9s6r4 ; Beta-lactamase (EC 3.5.2.6).
(from "lactxs_spt.pep")
TOIG of: q9s6r4 check: 345 from: 1 to: 381

ID Q9S6R4 PRELIMINARY; PRT; 381 AA.
AC Q9S6R4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Beta-lactamase (EC 3.5.2.6).
GN CMY-7.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMC 27;
RT "Three class C plasmid-mediated beta-lactamases from clinical isolates
of E. coli from Punjab, India."
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RU EMBL; AJ011291; CAB36900.1; -.
DR HSSP; P00811; 1C3B.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Hydrolase.
SQ SEQUENCE 381 AA; 41930 MW; F38E14AD038FD605 CRC64;

Q9S6R5 Length: 381 March 17, 2003 12:33 Type: P Check: 9759 ..
Found using 'narrow_ktxs' (swope073.key)

-----1
283 GDMYQGLGEMLMNPPLKADSIINGSDSKVALAALPAVEVNPAPPAVKASVWHTGSGTGF
333 340
343 GSYVAFIPQDGLIVMLANKSYNPVERVKAAMRILEKIQ

-----1
1 match found in sequence:
q9s6r5 ; Beta-lactamase (EC 3.5.2.6).
(from "lactxs_spt.pep")
TOIG of: q9s6r5 check: 9759 from: 1 to: 381

ID Q9S6R5 PRELIMINARY; PRT; 381 AA.
AC Q9S6R5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Beta-lactamase (EC 3.5.2.6).
GN CMY-6.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMC 37-76;
RT "Three class C plasmid-mediated beta-lactamases from clinical isolates
of E. coli from Punjab, India."
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RU EMBL; AJ011293; CAB36902.1; -.
DR HSSP; P00811; 1C3B.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Hydrolase.
SQ SEQUENCE 381 AA; 41930 MW; F38E14AD038FD605 CRC64;

Q9S6R5 Length: 381 March 17, 2003 12:33 Type: P Check: 9759 ..
Found using 'narrow_ktxs' (swope073.key)

-----1
283 GDMYQGLGEMLMNPPLKADSIINGSDSKVALAALPAVEVNPAPPAVKASVWHTGSGTGF
333 340
343 GSYVAFIPQDGLIVMLANKSYNPVERVKAAMRILEKIQ

-----1
1 match found in sequence:
q9x5c0 ; Beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q9x5c0 check: 5225 from: 1 to: 377

ID Q9X5C0 PRELIMINARY; PRT; 377 AA.
AC Q9X5C0;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Beta-lactamase.
GN AmpC.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El42;
RT "Characterization of AmpC type b-lactamases in clinical isolates of
cefotaxim-resistant Escherichia coli and Klebsiella pneumoniae."
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RU EMBL; AF124201; AAD28041.1; -.

```

DR HSSP; P00811; 1C3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 377 AA; 41500 MW; 6F1EF0A24C1275A7 CRC64;

Q9X5C0 Length: 377 March 17, 2003 12:33 Type: P Check: 5225
 Found using 'narrow_ktxs' (swope073.key)

279 GDMYQGLGEMLDWPNPDSIIINGSKKIVLAHPKAITPPTPAVRASVWVHKGTSTGF
 329 336

339 GSYVAFIPEKELGIYMLANKNYPNPVAVAAAMQILNALQ

 1 match found in sequence:
 q9x757 ; Beta-lactamase.
 (from "lactxs_spl.pep")
 TOIG of: q9x757 check: 8563 from: 1 to: 381

ID Q9X757 PRELIMINARY; PRT; 381 AA.
 AC Q9X757;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-lactamase.
 GN MIR-1.
 OS Klebsiella pneumoniae.
 OC Plasmid pmg230.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91158299; PubMed=1963529;
 RA Papanicolaou G.A., Medeiros A.A., Jacoby G.A.;
 RT "Novel plasmid mediated beta-lactamase (MIR-1) conferring resistance
 to oxytetracycline and alpha-methoxy-beta-lactams in clinical isolates of
 RT Klebsiella pneumoniae."
 RL Antimicrob. Agents Chemother. 34:2200-2209(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jacoby G.A., Tran J.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M37839; AAD22636.1; -.
 DR HSSP; P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Plasmid.
 SQ SEQUENCE 381 AA; 41171 MW; DD5B1D789C03142E CRC64;

Q9X757 Length: 381 March 17, 2003 12:33 Type: P Check: 8563
 Found using 'narrow_ktxs' (swope073.key)

283 GAMYQGLGEMLDWPNPDAKTYVGGSDKNKVALAPLPAVEVNPAPPAVKASVWVHKGTSTGF
 333 340

343 GSYVAFIPEKOLGIYMLANKSYNPVAVAYRILDALQ

 1 match found in sequence:
 q9x533 ; Beta-lactamase CMV-5.
 (from "lactxs_spl.pep")
 TOIG of: q9x533 check: 21 from: 1 to: 381

ID Q9X533 PRELIMINARY; PRT; 381 AA.
 AC Q9X533;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-lactamase CMV-5.
 GN BLACMV-5.
 OS Klebsiella oxytoca.
 OC Plasmid pTKH1.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=571;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KH11.
 RX MEDLINE=99277992; PubMed=10348751;
 RA Wu S.W., Dornbusch K., Kronvall G., Norgren M.;
 RT "Characterization and Nucleotide Sequence of a Klebsiella oxytoca
 RT Cryptic Plasmid Encoding a CMV-type beta-lactamase: Confirmation that
 RT the plasmid-mediated Cephamycinase Originated from the Citrobacter
 RT freundii AmpC beta-lactamase."
 RL Antimicrob. Agents Chemother. 43:1350-1357(1999).
 DR EMBL; Y17716; CAB50867.1; -.
 DR HSSP; P00811; 1C3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Plasmid.
 SQ SEQUENCE 381 AA; 42037 MW; 889EACCE51BC43F1 CRC64;

Q9X533 Length: 381 March 17, 2003 12:33 Type: P Check: 21
 Found using 'narrow_ktxs' (swope073.key)

283 GDMYQGLGEMLDWPNPLKADSIINGSDSKVALALPAVEVNPAPPAVKASVWVHKGTSTGF
 333 340

343 GSYVAFIPEKNLGIYMLANKSYNPVAVAYRILDALQ

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:00:00.05	00:00:04.00
Number of sequences searched:		217
Number of sequence hits:		37
Number of separate matches:		37
Number of sequence hits saved:		0

> 0 <
0/10 Intelligenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "narrow_pir" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "swope073.key":

1 narrow_ktxs (AA) ID narrow_ktxs AA preliminary pattern
vhtg5tg

Selected files:

File : lacktxs_pir.pep

-- Output Parameters --

Format Options:	File Options:	No
Nucleic acid code matching	Exact	No
Find non-matching hits only	Indirect file	No
Report key used	Sequence or key file	No
Note position of hit	List of hits	Yes
Display full annotations	Hit display	Yes
Sequence context	Name and annotations	Yes

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	NO

1 match found in sequence:

pkbq ; TOIG of: pnbkm check: 1311 from: 1 to: 381
(from "lacktxs_pir.pep")
TOIG of: pnbkm check: 1311 from: 1 to: 381

P1:PNKBM - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain

MMH1)

N:Alternate names: cephalosporinase

C:Species: Enterobacter cloacae

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 30-Jun-1993

C:Accession: S00406

R:Galleni, M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;

Frere, J.M.

Biochem. J. 250, 753-760, 1988

A>Title: Sequence and comparative analysis of three Enterobacter cloacae ampc
beta-lactamase genes and their products.

A:Reference number: S00404; MUID:88268750; PMID:3260487

A:Accession: S00406

A:Molecule type: DNA

A:Residues: 1-381 <GAL>

A:Cross-references: EMBL:X08082

C:Comment: This protein is a class C beta-lactamase.

C:Genetics:

A:Gene: ampc

C:Superfamily: Escherichia coli beta-lactamase

C:Keywords: antibiotic resistance; hydrolase

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-381/Product: beta-lactamase #status predicted <MAT>

F:84/Active site: Ser #status predicted

PNKBM Length: 381 March 17, 2003 12:10 Type: P Check: 1311
Found using 'narrow_ktxs' (swope073.key)

283 GSMYQGLGEMLNMPVEANTVVEGSDSKVALAPLVAEVNPPAPVKASWVHKGTSGGF 333 340

343 GSYVAFIPEKQIGIYMLANKSYNPARVEAAVHILEALQ

1 match found in sequence:

pkbq ; TOIG of: pnbq check: 735 from: 1 to: 381
(from "lacktxs_pir.pep")
TOIG of: pnbq check: 735 from: 1 to: 381

P1:PNKBP - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain

P99)

N:Alternate names: cephalosporinase

C:Species: Enterobacter cloacae

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Jun-1999

C:Accession: S00404

R:Galleni, M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;

Frere, J.M.

Biochem. J. 250, 753-760, 1988

A>Title: Sequence and comparative analysis of three Enterobacter cloacae ampc
beta-lactamase genes and their products.

A:Reference number: S00404; MUID:88268750; PMID:3260487

A:Accession: S00404

A:Molecule type: DNA

A:Residues: 1-381 <GAL>

A:Cross-references: EMBL:X07274; NID:942260; PIDN:CA30257.1; PID:942261

A>Note: part of this sequence, including the carboxyl end of the mature

protein, was confirmed by protein sequencing

C:Comment: This protein is a class C beta-lactamase.

C:Genetics:

A:Gene: ampc

C:Superfamily: Escherichia coli beta-lactamase

C:Keywords: antibiotic resistance; hydrolase

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-381/Product: beta-lactamase #status experimental <MAT>

F:84/Active site: Ser #status predicted

PNKBP Length: 381 March 17, 2003 12:10 Type: P Check: 735
Found using 'narrow_ktxs' (swope073.key)

283 GSMYQGLGEMLNMPVEANTVVEGSDSKVALAPLVAEVNPPAPVKASWVHKGTSGGF 333 340

343 GSYVAFIPEKQIGIYMLANKSYNPARVEAAVHILEALQ

1 match found in sequence:

pkbq ; TOIG of: pnbq check: 9705 from: 1 to: 375
(from "lacktxs_pir.pep")
TOIG of: pnbq check: 9705 from: 1 to: 375

P1:PNKBO - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain

O908R) (fragment)

N:Alternate names: cephalosporinase

C:Species: Enterobacter cloacae

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Jun-1999

C:Accession: S00405

R:Galleni, M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;

Frere, J.M.

Biochem. J. 250, 753-760, 1988

A>Title: Sequence and comparative analysis of three Enterobacter cloacae ampc
beta-lactamase genes and their products.

A:Reference number: S00404; MUID:88268750; PMID:3260487

A:Accession: S00405

A:Molecule type: DNA

A:Residues: 1-375 <GAL>

A:Cross-references: EMBL:X08081; NID:942611; PIDN:CA30878.1; PID:9757841

A>Note: parts of this sequence, including the amino and carboxyl ends of the
mature protein, were confirmed by protein sequencing

```

C:Comment: This protein is a class C beta-lactamase.
C:Genetics:
A:Gene: ampC
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-375/Product: beta-lactamase #status experimental <MAT>
F:78/Active site: Ser #status predicted

PKBQ Length: 375 March 17, 2003 12:10 Type: P Check: 9705
Found using 'narrow_ktxs' (swope073.key)

277 GSNYGLGEMLNWPEANTVEGSDSKVALPLPVEVNPAPVPKASVWHTKGTGCF
|-----|
327 334
337 GSYVAFPEKNIIGIYVANKSYNPVREAVRILEKIQ

-----
1 match found in sequence:
s08296 : TOIG of: s08296 check: 580 from: 1 to: 381
(from "lactxs_pir.pep")
TOIG of: s08296 check: 580 from: 1 to: 381

P1:S08296 - beta-lactamase (EC 3.5.2.6) precursor - Citrobacter freundii
(strain GN346)
N:Alternate names: cephalosporinase
C:Species: Citrobacter freundii
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Oct-1999
C:Accession: S08296; A60909; A27028; A24869
R:Takamoto, K.; Tachibana, K.; Yamazaki, N.; Ishii, Y.; Ujile, K.; Nishida,
N.; Sawai, T.
Eur. J. Biochem. 188, 15-22, 1990
A:Title: Role of lysine-67 in the active site of class C beta-lactamase from
Citrobacter freundii GN346.
A:Reference number: S08296; MUID:90201023; PMID:1969344
A:Accession: S08296
A:Molecule type: DNA
A:Residues: 1-381 <TSU>
A:Cross-references: GB:X51632; NID:q40457; PIDN:CAA35959.1; PID:q40458
A:Note: Part of this sequence was confirmed by amino acid sequencing
R:Sawai, T.; Yamaguchi, A.; Tsukamoto, K.
Rev. Infect. Dis. 10, 721-725, 1988
A:Title: Amino acid sequence, active-site residue, and effect of suicide
inhibitors on cephalosporinase of Citrobacter freundii GN346.
A:Reference number: A60909; MUID:89043488; PMID:3263684
A:Accession: A60909
A>Status: nucleic acid sequence not shown; not compared with conceptual
translation
A:Molecule type: DNA
A:Residues: 21-97, 'T', '99-381 <SAM>
R:Yamaguchi, A.; Adachi, H.; Sawai, T.
FEBS Lett. 218, 126-130, 1987
A:Title: Identification of the active site of Citrobacter freundii
beta-lactamase using dansyl-penicillin
A:Reference number: A27028; MUID:87247241; PMID:3496243
A:Accession: A27028
A:Molecule type: protein
A:Residues: 66-87 <YAM>
R:Lindberg, F.; Normark, S.
Eur. J. Biochem. 156, 441-445, 1986
A:Title: Sequence of the Citrobacter freundii OSG6 chromosomal ampC
beta-lactamase gene.
A:Reference number: A24869; MUID:86192473; PMID:3486121
A:Accession: A24869
A:Molecule type: DNA
A:Residues:
1-96, 'R', '98-142, 'G', '144, 'V', '146-149, 'E', '151-184, 'S', '186-223, 'L', '225-242, 'V', '244-
324, 'A', '326-367, 'A', '369-381 <LIN>
A:Cross-references: GB:X03866; NID:q40451; PIDN:CAA27494.1; PID:q40452
A:Experimental source: wild-type isolate OSG6

C:Genetics:
A:Gene: ampC
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-381/Product: beta-lactamase #status predicted <MAT>
F:84/Active site: Ser, Lys #status experimental

S08296 Length: 381 March 17, 2003 12:10 Type: P Check: 580
Found using 'narrow_ktxs' (swope073.key)

283 GDMYGLGEMLNWPLKADSIINGSDSKVALALPAVEVNPVPVPAKASVWHTKGTGCF
|-----|
333 340
343 GSYVAFPEKNIIGIYVANKSYNPVREAVRILEKIQ

-----
1 match found in sequence:
s39196 : TOIG of: s39196 check: 861 from: 1 to: 381
(from "lactxs_pir.pep")
TOIG of: s39196 check: 861 from: 1 to: 381

P1:S39196 - beta-lactamase (EC 3.5.2.6) - Escherichia coli
C:Species: Escherichia coli
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S39196
R:Fosberry, A.; Payne, D.J.; Lawlor, E.J.; Hodgson, J.E.
submitted to the EMBL Data Library, September 1993
A:Description: Cloning and sequence analysis of bla BIL-1: a plasmid mediated
class C beta-lactamase gene in Escherichia coli BS.
A:Reference number: S39196
A:Accession: S39196
A:Molecule type: DNA
A:Residues: 1-381 <FOS>
A:Cross-references: EMBL:X74512; NID:q433560; PIDN:CAA52618.1; PID:q433561
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: hydrolase
F:84/Active site: Ser #status predicted

S39196 Length: 381 March 17, 2003 12:10 Type: P Check: 861
Found using 'narrow_ktxs' (swope073.key)

283 GDMYGLGEMLNWPLKADSIINGSDTKVALAALPAVEVNPVPVPAKASVWHTKGTGCF
|-----|
333 340
343 GSYVAFPEKNIIGIYVANKSYNPVREAVRILEKIQ

-----
1 match found in sequence:
s44094 : TOIG of: s44094 check: 450 from: 1 to: 381
(from "lactxs_pir.pep")
TOIG of: s44094 check: 450 from: 1 to: 381

P1:S44094 - beta-lactamase (EC 3.5.2.6) - Citrobacter freundii
C:Species: Citrobacter freundii
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C:Accession: S44094
R:Bennet, P.M.; Damdinuren, E.; Jones, M.E.
submitted to the EMBL data library, December 1993
A:Reference number: S44094
A:Accession: S44094
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-381 <BEN>
A:Cross-references: EMBL:X76636; NID:q472907; PIDN:CAA54084.1; PID:q472908
C:Keywords: hydrolase

```

F:84/Active site: Ser #status predicted

S44094 Length: 381 March 17, 2003 12:10 Type: P Check: 450 ..
Found using 'narrow_ktxs' (swope073.key)

...

283 GEMVQGLGWEMLNMPVKADIVINGSDSKIALALPAVEVNPAPVAKASWVHKGTSGTF
333 340

343 GSYVAFPEKMLGIYMLANKSPNPVRVDAAMRIIEKIQ

1 match found in sequence:
S45109 ; TOIG of: S45109 check: 488 from: 1 to: 381
(from "lactixs_pir.pep")
TOIG of: S45109 check: 488 from: 1 to: 381

P1:S45109 - beta-lactamase (EC 3.5.2.6) precursor - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C:Accession: S45109
R:Tzouvelekis, L.S.; Tzelepi, E.; Mentis, A.F.
submitted to the EMBL Data Library, March 1994
A:Description: Nucleotide sequence of a plasmidic cephalosporinase gene
(bla-LAT-1) found in *Klebsiella pneumoniae*.
A:Reference number: S45109
A:Accession: S45109
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-381 <TZO>
A:Cross-references: EMBL:X78117; NID:9496632; PIDN:CAAS5007.1; PID:9496633
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: hydrolase
F:84/Active site: Ser #status predicted
S45109 Length: 381 March 17, 2003 12:10 Type: P Check: 488 ..
Found using 'narrow_ktxs' (swope073.key)

...

283 GDMVQGLGWEMLNMPVKADIVINGSDSKIALALPAVEVNPAPVAKASWVHKGTSGTF
333 340

343 GSYVAFPEKMLGIYMLANKSPNPVRVDAAMRIIEKIQ

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:01.00
Number of sequences searched:		34
Number of sequence hits:		7
Number of separate matches:		7
Number of sequence hits saved:		0

> 0 <
01/0 Intelligence
> 0 <

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Release 5.4

-- Outline of search "narrow_ags" --

Selected search type is key against sequence data banks or files.
Selected scope is sequence.
Selected sequence key from "swope073.key":
narrow_ktxs (AA) ID narrow_ktxs AA preliminary pattern

1 vnkgsstg
Selected files:

File : lacktxs_ags.pep

-- Output Parameters --

Format Options:	File Options:	
Nucleic acid code matching	Exact	No
Find non-matching hits only	No	No
Report key used	Yes	Yes
Note position of hit	Yes	Yes
Display full annotations	Yes	Yes
Sequence context	50	Yes

-- Run Parameters --

Run mode	Batch
Time to start comparison	NO
Notify at end of run	NO

1 match found in sequence:

aaui1993 ; Enterobacter cloacae beta-lactamase-like (cephalosporinase) protein
(from "lacktxs_ags.pep")
TOIG of: aaui1993 check: 524 from: 1 to: 395

ID AAUI1993 standard; Protein; 361 AA.
XX
AC AAUI1993;
DT 09-APR-2002 (first entry)
XX
DE Enterobacter cloacae beta-lactamase-like (cephalosporinase) protein.
XX
KW Polymer crossover location; crossover recombination; hybrid biopolymer;
KM directed evolution of polymer; beta-lactamase-like protein;
XX cephalosporinase.
OS Enterobacter cloacae.
XX
PN WO200190346-A2.
PD 29-NOV-2001.
PF 23-MAY-2001; 2001WO-US16831.
XX
PR 23-MAY-2000; 2000US-207048P.
PR 27-SEP-2000; 2000US-235960P.
PR 13-APR-2001; 2001US-283567P.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Wang Z, Voigt CA, Mayo SL, Arnold FH;
XX
DR WPI; 2002-122019/16.
XX
PT Selecting a crossover locations in biopolymers, useful for particularly

PT useful designing, engineering and generating new proteins and genes
PT with useful properties, by determining the crossover disruption
PT profiles of biopolymers -

Examples: Fig 3; 139pp; English.

CC The present invention relates to methods for identifying crossover
CC locations in a polymer including nucleic acids and proteins. The
CC method involves selecting a crossover location in a first biopolymer
CC having a first polymer sequence, for recombination with one or more
CC second biopolymers each having its own polymer sequence. The method
CC comprises determining a crossover disruption related to the number of
CC coupling interactions disrupted in the crossover mutant represented
CC by a data structure. The method is useful for the directed evolution
CC of polymers, including directed evolution of nucleic acids and proteins.
CC The methods are particularly useful for designing, engineering and
CC generating hybrid biopolymers. The methods are also useful for
CC accelerating the production of new proteins and genes with novel and
CC useful properties. The present sequence representing Enterobacter
CC cloacae beta-lactamase-like (cephalosporinase) protein is used in
CC crossover studies in the methods of the present invention.

XX Sequence 361 AA;

AAUI1993 length: 395 March 17, 2003 14:16 Type: N Check: 524 ..
Found using 'narrow_ktxs' (swope073.key)

263 GSNYGLGWMELNWPVEANTVSGSDSKVALAPLPAEYVNPAPPVKASWVHKTGSTGSP
313 320

323 GSYVAFIPEKQIGIVMLANTSYNPARVEAAYHILEALQ

1 match found in sequence:

aaui1994 ; Citrobacter freundii beta-lactamase-like (cephalosporinase) protein
(from "lacktxs_ags.pep")
TOIG of: aaui1994 check: 1638 from: 1 to: 395

ID AAUI1994 standard; Protein; 361 AA.
XX
AC AAUI1994;
DT 09-APR-2002 (first entry)
XX
DE Citrobacter freundii beta-lactamase-like (cephalosporinase) protein.
XX
KW Polymer crossover location; crossover recombination; hybrid biopolymer;
KM directed evolution of polymer; beta-lactamase-like protein;
XX cephalosporinase.
XX
OS Citrobacter freundii.
XX
PN WO200190346-A2.
PD 29-NOV-2001.
PF 23-MAY-2001; 2001WO-US16831.
XX
PR 23-MAY-2000; 2000US-207048P.
PR 27-SEP-2000; 2000US-235960P.
PR 13-APR-2001; 2001US-283567P.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Wang Z, Voigt CA, Mayo SL, Arnold FH;
XX
DR WPI; 2002-122019/16.
XX
PT Selecting a crossover locations in biopolymers, useful for particularly
PT useful designing, engineering and generating new proteins and genes

PT with useful properties, by determining the crossover disruption
 PT profiles of biopolymers -
 XX
 PS Examples: Fig 3; 139pp; English.
 CC The present invention relates to methods for identifying crossover
 CC locations in a polymer including nucleic acids and proteins. The
 CC method involves selecting a crossover location in a first biopolymer
 CC having a first polymer sequence, for recombination with one or more
 CC second biopolymers each having its own polymer sequence. The method
 CC comprises determining a crossover disruption related to the number of
 CC coupling interactions disrupted in the crossover mutant represented
 CC by a data structure. The method is useful for the directed evolution
 CC of polymers, including directed evolution of nucleic acids and proteins.
 CC The methods are particularly useful for designing, engineering and
 CC generating hybrid biopolymers. The methods are also useful for
 CC accelerating the production of new proteins and genes with novel and
 CC useful properties. The present sequence representing Citrobacter
 CC freundii beta-lactamase-like (cephalosporinase) protein is used in
 CC crossover studies in the methods of the present invention.
 XX
 SQ Sequence 361 AA;
 AAM11994 Length: 395 March 17, 2003 14:16 Type: N Check: 1638 ..
 Found using 'narrow_ktxs' (swope073.key)

263 GDMYGLGWEMLNMPLEKADSLINGSKVALALPAVEVNPAPPAVKASVWHTGSTGGR
 313 320

323 GSYVAFVPEKNLGIWMLANKSYNPAPRVKAAWRIELEKIQ

1 match found in sequence:
 aaw87786; Fusion protein L49-sfv-bl.
 (from "lactxs_ags.pep")
 ToIG of: aaw87786 check: 5303 from: 1 to: 667

ID AAM87786 standard; Protein; 633 AA.
 XX
 AC AAM87786;
 XX
 DT 11-MAY-1999 (first entry)
 XX
 DE Fusion protein L49-sfv-bl.
 XX
 KW Fusion protein; antibody; light chain; heavy chain; variable region;
 KW melanoma-associated antigen; beta-lactamase; cytotoxic agent; prodrg;
 KW tumour cell; primer; PCR; amplification; ss.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Enterobacter cloacae.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /note="PelB leader sequence"
 FT 23..141
 FT Domain
 FT /note="L49 heavy chain variable region"
 FT 142..159
 FT Region
 FT /note="spacer peptide 218"
 FT 160..272
 FT Domain
 FT /note="L49 light chain variable region"
 FT 273..633
 FT /note="beta-lactamase"
 XX
 PN WO9850432-A1.
 XX
 PD 12-NOV-1998.
 XX
 PF 30-APR-1998; 98WO-US08840.

PR 30-APR-1998; 98US-0070637.
 PR 07-MAY-1997; 97US-0045888.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Senter PD, Siemers NO, Yarnold S;
 XX
 DR WPI: 1999-070092/06.
 XX N-PSDB; AAV99657.
 XX
 PT New fusion polypeptide of antibody variable regions and
 PT beta-lactamase - are targetted to melanoma-associated antigens and
 used to generate cytotoxic agents from prodrgs, at tumour cells
 XX
 PS Claim 10; Fig 4A-B; 50pp; English.
 XX
 CC The invention relates to a new fusion polypeptide comprising an antibody
 CC light and heavy chain variable regions specific for a
 CC melanoma-associated antigen (Ag) linked to a beta-lactamase (bl). This
 CC sequence represents the fusion protein L49-sfv-bl which comprises the
 CC heavy and light chain variable regions from the antibody L49 (targeted to
 CC the melanotransferrin protein p97) linked, via the spacer peptide 218
 CC (AAM87785), to the Enterobacter cloacae beta-lactamase enzyme. The
 CC fusion protein is used to deliver cytotoxic agents to tumour cells: it
 CC binds to a tumour cell Ag and converts an administered prodrg to the
 CC active form.
 XX
 SQ Sequence 633 AA;
 AAM87786 Length: 667 March 17, 2003 14:16 Type: N Check: 5303 ..
 Found using 'narrow_ktxs' (swope073.key)

535 GSMYGLGWEMLNMPVEANTVETISFGVALALPAVEVNPAPPAVKASVWHTGSTGGR
 585 592

595 GSYVAFPEKQIGIWMANTSYNPAPRVKAAWRIELEKIQ

-- Search Statistics --

Times:	CPU	Total Elapsed
00:00:00.02		00:00:01.00

Number of sequences searched:	151
Number of sequence hits:	3
Number of separate matches:	3
Number of sequence hits saved:	0

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```
-- Outline of search "narrow_sp" --
```

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "swope073.key":

```
selected sequence key from "swope073.key":
```

Selected files:

File : lacktxs_sp.pep

```
-- Output Parameters --
```

Format Options:		File Options:	
Nucleic acid code matching	Exact	Indirect file	No
Find non-matching hits only	No	Sequence or key file	No
Report key used	Yes	List of hits	Yes
Note position of hit	Yes	Hlt display	Yes
Display full annotations	Yes	Name and annotations	yes
Sequence context	50		

```
-- Run Parameters --
```

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

1 match found in sequence:
 ampcciflr | Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase)
 (from "lactxs.sp.pep")
 TOIG of: ampcciflr check: 382 from: 1 to: 381

ID	AMPC_CITFR	STANDARD;	PRT;	381 AA.
AC	P05193;			
DT	13-AUG-1987	(Rel. 05, Created)		
DT	13-AUG-1987	(Rel. 05, Last sequence update)		
DT	15-DEC-1998	(Rel. 37, Last annotation update)		
DE	Beta-lactamase precursor (EC 3.5.2.6) (cephalosporinase).			
GN	AMPC OR BLAC.			
OS	Citrobacter freundii.			
OC	Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae; Citrobacter.			
OX	NCBI_TaxID=546;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=OS60;			
RX	MEDLINE=66192473; PubMed=3486121;			
RA	Lindberg F., Normark S.,			
RT	"Sequence of the Citrobacter freundii OS60 chromosomal ampc beta-			
RT	lactamase gene.";			
RL	Eur. J. Biochem. 156:441-445(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=GN346;			
RX	MEDLINE=90201023; PubMed=1969344;			
RA	Tsukamoto K., Tachibana K., Yamazaki N., Ishii Y., Ujile K.,			
RA	Nishida N., Sawai T.;			
RT	"Role of lysine-67 in the active site of class C beta-lactamase from			
RT	Citrobacter freundii GN346.";			
RL	Eur. J. Biochem. 188:15-22(1990).			
RN	[3]			
RP	SEQUENCE OF 66-87.			
RX	MEDLINE=67247241; PubMed=3496243;			

DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase).
 GN AmpC.
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-P99, 0908R, and MHNI;
 RX MEDLINE=88268750; PubMed=3260487;
 RA Galleni M., Lindberg F., Normark S., Cole S., Honore N., Joris B.,
 RA Frere J.-M.;
 RT "Sequence and comparative analysis of three Enterobacter cloacae ampC
 RT beta-lactamase genes and their products.";
 RL Biochem. J. 250:753-760(1988).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RC STRAIN-P99;
 RX MEDLINE=94068583; PubMed=8248237;
 RA Lobkovsky E., Moews P.C., Liu H., Zhao H., Frere J.-M., Knox J.R.;
 RT "Evolution of an enzyme activity: crystallographic structure at 2-A
 RT resolution of cephalosporinase from the ampC gene of Enterobacter
 RT cloacae P99 and comparison with a class A penicillinase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:11257-11261(1993).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RC STRAIN-P99;
 RX MEDLINE=94263990; PubMed=8204611;
 RA Lobkovsky E., Billings E.M., Moews P.C., Rahl J., Pratt R.F.,
 RA Knox J.R.;
 RT "Crystallographic structure of a phosphonate derivative of the
 RT Enterobacter cloacae P99 cephalosporinase: mechanistic interpretation
 RT of a beta-lactamase transition-state analog.";
 RL Biochemistry 33:6762-6772(1994).
 CC -!- FUNCTION: THIS PROTEIN IS A SERINE BETA-LACTAMASE WITH A SUBSTRATE
 CC SPECIFICITY FOR CEPHALOSPORINS.
 CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 CC amino acid.
 CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
 CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN P99.
 CC -!- SIMILARITY: BELONGS TO THE CLASS-C BETA-LACTAMASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb.ch).
 CC -----
 CC EMBL: X07274; CA30257.1; -;
 DR EMBL: X08082; CA30879.1; -;
 DR EMBL: X08081; CA30878.1; -;
 DR PIR: S00404; PIRBP.
 DR PIR: S00405; PIRBO.
 DR PIR: S00406; PIRBM.
 DR PDB: 1BLS; 08-MAY-95.
 DR PDB: 2BLT; 26-JAN-95.
 DR MEROPS: S12.UNM; -;
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Hydrolase; Antibiotic resistance; Periplasmic; Signal; 3D-structure.
 FT SIGNAL 1 20
 FT CHAIN 21 381 BETA-LACTAMASE.
 FT ACT SITE 84 84
 FT BINDING 335 337
 FT VARIANT 3 3
 FT VARIANT 14 14 R -> I (IN STRAIN MHNI).
 FT VARIANT 21 21 T -> A (IN STRAIN MHNI).
 FT VARIANT 21 21

FT VARIANT 36 36 I -> V (IN STRAINS MHNI AND Q980R).
 FT VARIANT 58 58 P -> S (IN STRAIN MHNI).
 FT VARIANT 108 108 A -> P (IN STRAINS MHNI AND Q980R).
 FT VARIANT 152 152 L -> V (IN STRAIN Q980R).
 FT VARIANT 262 262 N -> K (IN STRAIN MHNI).
 FT VARIANT 319 319 A -> V (IN STRAIN Q980R).
 FT VARIANT 362 362 T -> K (IN STRAIN MHNI).
 SQ SEQUENCE 381 AA; 41301 MM; 90F56ABAF07AA304 CRC64;
 AMPC_ENTCL Length: 381 March 17, 2003 12:16 Type: P Check: 735
 Found using 'narrow_ktxs' (swope073.key)
 ...
 263 GSNYQGLGEMLNPNVEANTVYEGSDSKVALPLPAVEVNPAPPVKASVYHKGSGCGP
 343 GSYVAFIPEKQIGIVMLANTSYNPAPARVEAAYHILEALQ

 -- Search Statistics --
 Times: CPU Total Elapsed
 00:00:00.00 00:00:00.00
 Number of sequences searched: 30
 Number of sequence hits: 2
 Number of separate matches: 2
 Number of sequence hits saved: 0

> 0 <
01/10 Intelligenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "ktxs_aggs" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence. "swope073.key":

Selected sequence key from "swope073.key":

KTXS (AA) ID KTXS AA preliminary pattern

1 followed by

2 kt

2 any character

2 s

Selected files:

File : lacktxs_aggs.pep

-- Output Parameters --

Format Options:

Nucleic acid code matching Exact

Find non-matching hits only No

Report key used Yes

Note position of hit Yes

Display full annotations Yes

Sequence context 50

File Options:

Indirect file

Sequence or key file

List of hits

Hit display

Name and annotations

50

NO
NO
Yes
Yes
Yes
Yes

-- Run Parameters --

Run mode

Time to start comparison

Notify at end of run

Batch

now

NO

1 match found in sequence:

aarl0145 ; Cephalosporin antibiotic biosynthetic enzyme #1.

(from "lacktxs_aggs.pep")

TOIG of: aarl0145 Check: 3233 from: 1 to: 3756

ID AAR10145 standard; Protein: 3722 AA.

AC AAR10145;

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DT 27-MAR-1991 (first entry)

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Cephalosporin antibiotic biosynthetic enzyme #1.

cephalosporin; antibiotic;

S-(L-alpha-aminoadipyl)-L-cysteiny-D-; valine synthetase;

isopenicillin N synthetase; isopenicillin N epimerase;

deacetoxycephalosporin C synthetase; beta-lactamase;

deacetoxycephalosporin C hydroxylase.

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DR N-PSDB; AAQ10190.

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1 match found in sequence:

aarl0692 ; Cephalosporin antibiotic biosynthetic enzyme #6.

(from "lacktxs_aggs.pep")

TOIG of: aarl0692 Check: 3605 from: 1 to: 419

ID AAR10692 standard; Protein: 385 AA.

AC AAR10692;

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PS Disclosure; Fig 13; 67pp; Japanese.

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1077 LESHRRHLDYWAQACERLSEKGFAGLINQNNRYKVFGEYDRAEHRITKTSVDPCT
1127

1137 AAIKDCAGHRVTLASVLOFAMHKLPLAIGSPVTWGTIVISGR

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CC isolated from *L. lactamgenus* and comprising the genes for the
 CC cephalosporin biosynthetic enzymes listed in the KEYWORDS. Plasmids
 CC containing at least one of ORF's 1-9 can be used to transform
 CC microbes, such as bacteria or yeast.
 CC See also AAQ10191-2.

Sequence 385 AA:

AAK10692 Length: 419 March 17, 2003 14:16 Type: N Check: 3605
 Found using 'KTXS' (swope073.key)

285 MTQGLVWEQQLPYPASETSLQANSSOKVFESENAVALTPPPPOANVLINTGSTRGFGA
 335

345 YVAFNPARRKIGIVLLMNRSPMDGRKLAHTLLDTAGSMAR

 1 match found in sequence:
 aar13835 ; Mutant signal peptide A2d.
 (from "lactxs_ags.pep")

TOTG of: aar13835 Check: 1472 from: 1 to: 65

ID AAR13835 standard; Protein: 31 AA.

AC AAR13835;

DT 14-NOV-1991 (first entry)

DE Mutant signal peptide A2d.

SWase I; expression; export; signal peptide; processing.

OS Bacillus subtilis.

PN EP444759-A.

PD 04-SEP-1991.

PF 28-FEB-1991; 91EP-0200431.

PR 24-DEC-1990; 90EP-0203509.

PR 28-FEB-1990; 90EP-0200477.

PR 28-FEB-1991; 91EP-0200431.

PA (KONN) GIST-BROCADES NV.

PI Van Dijk JM, Smith HE, Bron S, Quax WJ;

DR WPI; 1991-261526/36.

DR N-PSDB; AAQ13366.

PT DNA sequence encoding signal peptidase - for cloning and

PT over-expression of leader peptidase gene for enhanced rate of

PT protein processing

PS Disclosure; Page 24; 51pp; English.

XX The signal peptide A2d. from *B. subtilis* (EP-244-42) contd. a

CC "pro-like" long ORF between the hydrophobic core and the fusion point

CC with the target protein. To investigate whether this very hydrophobic

CC "pro-like" region plays a role in protein export, the polypeptide

CC region of 37 amino acids starting from Ala28 to Leu64 were deleted by

CC oligonucleotide-directed site-specific mutagenesis.

CC Data (reduced processing rate) have indicated that the region was

CC important for efficient processing of pre(A2)-alpha-amylase and

CC pre(A2)-beta-lactamase, most likely due to the presence of a potential

CC processing site at Ala30, which was removed with the deletion in A2d.

CC See also AAQ13365-68.

CC Sequence 31 AA;

XX

SQ

AAK13835 Length: 65 March 17, 2003 14:16 Type: N Check: 1472
 Found using 'KTXS' (swope073.key)

1 VRKSLITLGLAVYIGTSFLIPTSTKSTSTA
 26 29

 1 match found in sequence:

aar22954 ; Promoter/secretion promoting signal sequence from PKTH1801.

(from "lactxs_ags.pep")

TOTG of: aar22954 Check: 3493 from: 1 to: 114

ID AAR22954 standard; Protein: 80 AA.

AC AAR22954;

DT 15-OCT-1992 (first entry)

DE Promoter/secretion promoting signal sequence from PKTH1801.

SW Probe-vector; secretion; signal; promoter; plasmid; expression;

heterologous; homologous; *E. coli*; Gram-positive bacteria;

TEM; beta-lactamase; TEM-bla.

OS Lactobacillus lactis subsp. lactis.

PN Key Location/Qualifiers

PD Region 77..80

PD WO9204451-A.

PD 19-MAR-1992.

PF 30-AUG-1990; 90WO-FR00204.

PR 30-AUG-1990; 90WO-F100204.

PR (GENE-) GENESIT OY.

PA Palva I, Sibakov M, Koivula T, Von Wright A;

PI WPI; 1992-131815/16.

DR N-PSDB; AAQ23886.

DR Promoter probe vectors for protein expression - replicable in *E.*

PT coli, *B. subtilis*, *Lactococci* and *Lactobacillus*

PS Disclosure; Fig 17; 70pp; English.

XX The three reading frames of the sequence represented in AAQ23886 were

CC matched with the known reading frame of beta-lactamase, in order to

CC determine the correct reading frame. The deduced amino acid

CC sequence of one reading frame is given here, and is an exact

CC reproduction of the sequence given in the specification, i.e.

CC including the three X's which are encoded by stop codons.

CC Promoter probe-vectors PKTH1734, PKTH1736 and PKTH1750 were used to

CC clone and sequence previously unknown and undescribed *L. lactis* subsp.

CC lactis promoter and promoter/secretion signal promoting nucleotide

CC sequences. These sequences are contained in PKTH1816 (AAQ23878),

CC PKTH1817 (AAQ23879), PKTH1820 (AAQ23880), PKTH1874 (AAQ23881), PKTH1789

CC (AAQ23882), PKTH1797 (AAQ23883), PKTH1798 (AAQ23884), PKTH1799

CC (AAQ23885), PKTH1801 (AAQ23886), PKTH1821 (AAQ23887). The sequences may

CC be beneficially incorporated into plasmids, by means of which it is

CC possible to achieve enhanced heterologous (and homologous) protein

CC expression in *E. coli* and, esp., in Gram-positive bacteria.

CC Sequence 80 AA;

XX

SQ

AAK22954 Length: 114 March 17, 2003 14:16 Type: N Check: 3493
 Found using 'KTXS' (swope073.key)


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PT Selecting a crossover locations in biopolymers, useful for particularly
PT useful designing, engineering and generating new proteins and genes
PT with useful properties, by determining the crossover disruption
PT profiles of biopolymers -
XX
XX Examples; Fig 3; 139pp; English.
XX
CC The present invention relates to methods for identifying crossover
CC locations in a polymer including nucleic acids and proteins. The
CC method involves selecting a crossover location in a first biopolymer
CC having a first polymer sequence, for recombination with one or more
CC second biopolymers each having its own polymer sequence. The method
CC comprises determining a crossover disruption related to the number of
CC coupling interactions disrupted in the crossover mutant represented
CC by a data structure. The method is useful for the directed evolution
CC of polymers, including directed evolution of nucleic acids and proteins.
CC The methods are particularly useful for designing, engineering and
CC accelerating the production of new proteins and genes with novel and
CC useful properties. The present sequence representing Enterobacter
CC cloacae beta-lactamase-like (cephalosporinase) protein is used in
CC crossover studies in the methods of the present invention.
XX
XX Sequence 361 AA;
SQ
AAU11993 Length: 395 March 17, 2003 14:16 Type: N Check: 524 ..
Found using 'KTXS' (swope073.key)

...

265 MYGIGEMLNMPVEANTVVEGSDSKVALAPLPAVEVNPAPPAVKASWVHTGSGFGS
|---|
315
325 YVAFPEKQIGIVMLANTSTPNPARVAAYHILEALO

-----
1 match found in sequence:
aa11994 : Citrobacter freundii beta-lactamase-like (cephalosporinase) protein
(from "lacks.ags.pep")
TOIG of: aa11994 Check: 1638 from: 1 to: 395

ID AAU11994 standard; Protein: 361 AA.
XX
XX AC AAU11994;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Citrobacter freundii beta-lactamase-like (cephalosporinase) protein.
XX
XX KW Polymer crossover location; crossover recombination; hybrid biopolymer;
XX directed evolution of polymer; beta-lactamase-like protein;
XX cephalosporinase.
XX
XX OS Citrobacter freundii.
XX
XX PN WO200190346-A2.
XX
XX PD 29-NOV-2001.
XX
XX PF 23-MAY-2001; 2001WO-US16831.
XX
XX PR 23-MAY-2000; 2000US-207048P.
XX 27-SEP-2000; 2000US-235960P.
XX 13-APR-2001; 2001US-283567P.
XX
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
XX PI Wang Z, Voigt CA, Mayo SL, Arnold FH;
XX
XX DR WPI; 2002-122019/16.
XX
XX PT Selecting a crossover locations in biopolymers, useful for particularly

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PT useful designing, engineering and generating new proteins and genes
PT with useful properties, by determining the crossover disruption
PT profiles of biopolymers -
XX
XX Examples; Fig 3; 139pp; English.
XX
CC The present invention relates to methods for identifying crossover
CC locations in a polymer including nucleic acids and proteins. The
CC method involves selecting a crossover location in a first biopolymer
CC having a first polymer sequence, for recombination with one or more
CC second biopolymers each having its own polymer sequence. The method
CC comprises determining a crossover disruption related to the number of
CC coupling interactions disrupted in the crossover mutant represented
CC by a data structure. The method is useful for the directed evolution
CC of polymers, including directed evolution of nucleic acids and proteins.
CC The methods are particularly useful for designing, engineering and
CC accelerating the production of new proteins and genes with novel and
CC useful properties. The present sequence representing Citrobacter
CC freundii beta-lactamase-like (cephalosporinase) protein is used in
CC crossover studies in the methods of the present invention.
XX
XX Sequence 361 AA;
SQ
AAU11994 Length: 395 March 17, 2003 14:16 Type: N Check: 1638 ..
Found using 'KTXS' (swope073.key)

...

265 MYGIGEMLNMPLEKADSIINGSDSKVALAPLPAVEVNPAPPAVKASWVHTGSGFGS
|---|
315
325 YVAFPEKMLGIVMLANKSTPNPARVAAYHILEALO

-----
2 matches found in sequence:
aa11996 : Klebsiella pneumoniae beta-lactamase-like (cephalosporinase) protei
(from "lacks.ags.pep")
TOIG of: aa11996 Check: 6604 from: 1 to: 393

ID AAU11996 standard; Protein: 359 AA.
XX
XX AC AAU11996;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Klebsiella pneumoniae beta-lactamase-like (cephalosporinase) protein.
XX
XX KW Polymer crossover location; crossover recombination; hybrid biopolymer;
XX directed evolution of polymer; beta-lactamase-like protein;
XX cephalosporinase.
XX
XX OS Klebsiella pneumoniae.
XX
XX PN WO200190346-A2.
XX
XX PD 29-NOV-2001.
XX
XX PF 23-MAY-2001; 2001WO-US16831.
XX
XX PR 23-MAY-2000; 2000US-207048P.
XX 27-SEP-2000; 2000US-235960P.
XX 13-APR-2001; 2001US-283567P.
XX
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
XX PI Wang Z, Voigt CA, Mayo SL, Arnold FH;
XX
XX DR WPI; 2002-122019/16.
XX
XX PT Selecting a crossover locations in biopolymers, useful for particularly
PT useful designing, engineering and generating new proteins and genes

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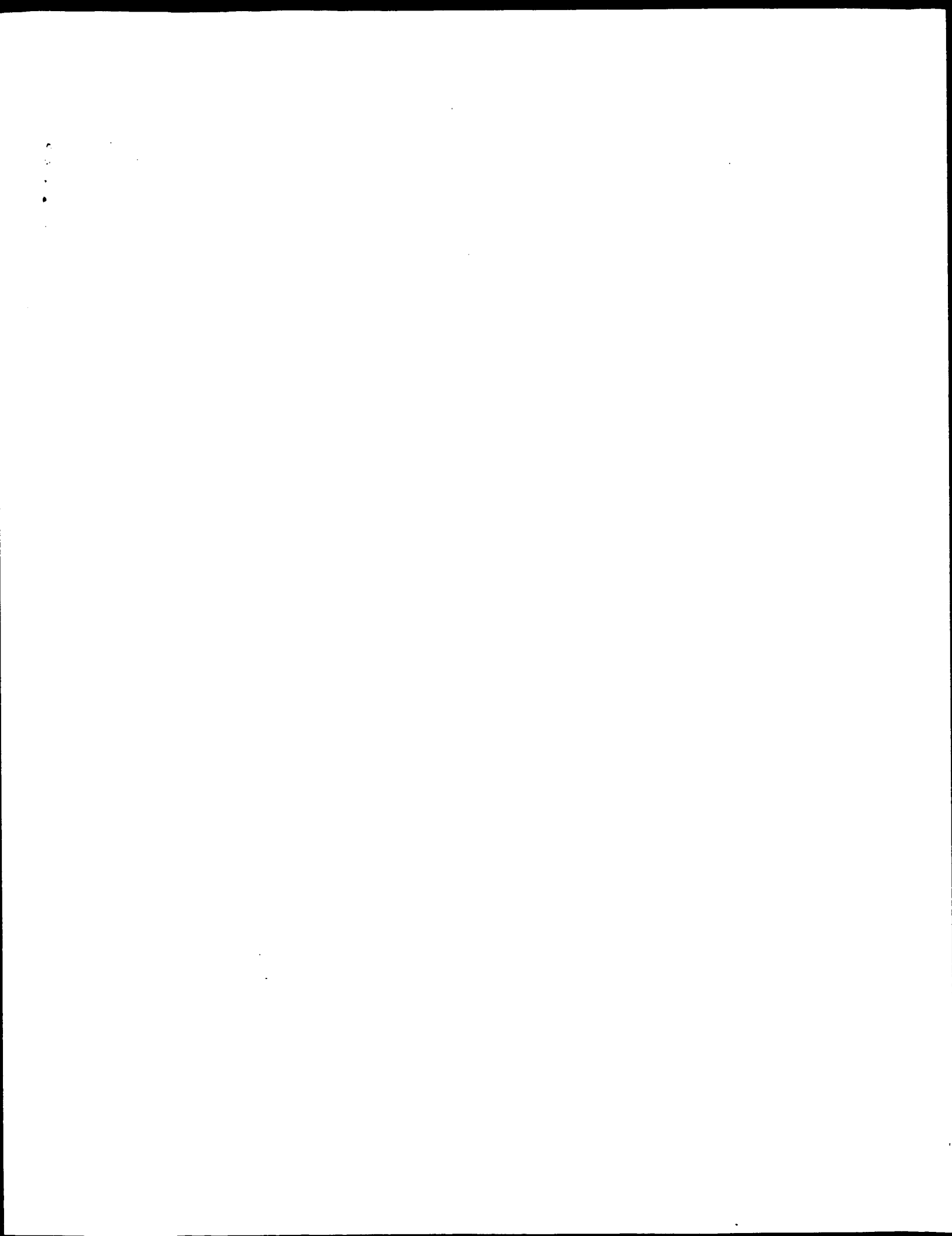
PT with useful properties, by determining the crossover disruption
PT profiles of biopolymers -
XX
XX
PS Examples: Fig 3; 139pp; English.
XX
CC The present invention relates to methods for identifying crossover
CC locations in a polymer including nucleic acids and proteins. The
CC method involves selecting a crossover location in a first biopolymer
CC having a first polymer sequence, for recombination with one or more
CC second biopolymers each having its own polymer sequence. The method
CC comprises determining a crossover disruption related to the number of
CC coupling interactions disrupted in the crossover mutant represented
CC by a data structure. The method is useful for the directed evolution
CC of polymers, including directed evolution of nucleic acids and proteins.
CC The methods are particularly useful for designing, engineering and
CC generating hybrid biopolymers. The methods are also useful for
CC accelerating the production of new proteins and genes with novel and
CC useful properties. The present sequence representing Klebsiella
CC pneumoniae beta-lactamase-like (cephalosporinase) protein is used in
CC crossover studies in the methods of the present invention.
XX
SQ Sequence 359 AA:
AAU11996 Length: 393 March 17, 2003 14:16 Type: N Check: 6604 ..
Found using 'KTXS' (swope073.key)
...
174 MSQTLPLKLGHHHTYIQVPESAIANVAYGKEDKPVRTFQVLAEMAYGKIKGSDLLKLF
|---|
224
234 TEANMGYGDALAKTRIALTHGTFYSGDMQGLGMSYAPLDTQALLAGSPAVSFQA
|---|
294 NPVTRPAVPKANGGEORLYNKGTSGGFGAYVAFVPAFGIAIYMLANRNPPIEARVKAHA
313
354 ILSQLA
-----
1 match found in sequence:
aaw87786 ; Fusion protein L49-sFv-DL.
(from "ktxs_ags.pep")
TOIG of: aaw87786 Check: 5303 from: 1 to: 667
ID AAW87786 standard; Protein; 633 AA.
XX
XX AAW87786;
AC
XX
XX 11-MAY-1999 (first entry)
DT
XX
DE Fusion protein L49-sFv-DL.
XX
XX Fusion protein; antibody; light chain; heavy chain; variable region;
KW melanoma-associated antigen; beta-lactamase; cytotoxic agent; produg;
KW tumour cell; primer; PCR; amplification; ss.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Enterobacter cloacae.
XX
XX Key
FH Location/Qualifiers
FH Peptide
FT 1..22
FT /note="PeLB leader sequence"
FT Domain
FT 23..141
FT /note="L49 heavy chain variable region"
FT Region
FT 142..159
FT /note="spacer peptide 218"
FT 160..272
FT /note="L49 light chain variable region"
FT 273..633
FT /note="beta-lactamase"
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PN WO9850432-A1.
XX
XX 12-NOV-1998.
PD
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XX 30-APR-1998; 98WO-US08840.
PF
XX
XX 30-APR-1998; 98US-0070637.
PR 07-MAY-1997; 97US-0045888.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Senter PD, Siemers NO, Yarnold S;
PI WPI: 1999-070092/06.
DR N-PSDB: AAV99657.
XX
XX New fusion polypeptide of antibody variable regions and
PT beta-lactamase - are targeted to melanoma-associated antigens and
PT used to generate cytotoxic agents from produgs, at tumour cells
XX
XX Claim 10; Fig 4A-B; 50pp; English.
PS
XX
XX The invention relates to a new fusion polypeptide comprising an antibody
CC light and heavy chain variable regions specific for a
CC melanoma-associated antigen (Ag) linked to a beta-lactamase (BL). This
CC sequence represents the fusion protein L49-sFv-DL which comprises the
CC heavy and light chain variable regions from the antibody L49 (targeted to
CC the melanotransferrin protein p97) linked, via the spacer peptide 218
CC (AAW87785), to the Enterobacter cloacae beta-lactamase enzyme. The
CC fusion protein is used to deliver cytotoxic agents to tumour cells; it
CC binds to a tumour cell Ag and converts an administered produg to the
CC active form.
XX
SQ Sequence 633 AA:
AAW87786 Length: 667 March 17, 2003 14:16 Type: N Check: 5303 ..
Found using 'KTXS' (swope073.key)
...
537 MYOGLGEMLMNPVEANTVETSGFNALAPLPVAEVPAPAPYKASWVHKGTSGGFGS
|---|
587
597 YVAFIPEKQIGIVMLANTSYNPAPRVAEAAHIILEALO
-- Search Statistics --
Times: CPU Total Elapsed
00:00:00.02 00:00:00.00
Number of sequences searched: 151
Number of sequence hits: 9
Number of separate matches: 10
Number of sequence hits saved: 0

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> 0 <
01/00 Intelligenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "ktxs_pir" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "swope073.key":

KTXS (AA) ID KTXS AA preliminary pattern
1 followed by
2 kt
2 any character
2 s

Selected files:

File : lacktxs_pir.pep

-- Output Parameters --

Format Options:	File Options:
Nucleic acid code matching	Exact
Find non-matching hits only	No
Report key used	Yes
Note position of hit	Yes
Display full annotations	Yes
Sequence context	50

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	NO

1 match found in sequence:

a55792 ; TOIG of: a55792 check: 1582 from: 1 to: 300
(from "lacktxs_pir.pep")
TOIG of: a55792 check: 1582 from: 1 to: 300

P1:A55792 - beta-lactamase (EC 3.5.2.6) precursor - Proteus vulgaris
C:Species: Proteus vulgaris

C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 20-Jun-2000
C:Accession: A55792

R:Tamaki, M.; Nakaga, M.; Sawai, T.

Biochemistry 33, 10200-10206, 1994

A:Title: Replacement of serine 237 in class A beta-lactamase of Proteus
vulgaris modifies its unique substrate specificity.

A:Reference number: A55792; MUID:94339110; PMID:8060986

A:Accession: A55792

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-300 <TMM>

A:Cross-references: GB:D29982; NID:9484056; PIDN:BAA06252.1; PID:9599572

C:Superfamily: beta-lactamase I

C:Keywords: hydrolase

F:46/Active site: Ser #status predicted

A55792 Length: 300 March 17, 2003 12:10 Type: P Check: 1582 ..
Found using 'KTXS' (swope073.key)

---|

189 IMAKSIQALTLGDALGOSQROLVTVLKNGTGTGDSIRKGLPKHNVGKTSQSGYGT
239

249 NDIIVMPENHAPLILVYFTQOEQNAKRYKRIIAKAEIVTKE

...

1 match found in sequence:

ag2934 ; TOIG of: ag2934 check: 9987 from: 1 to: 385
(from "lacktxs_pir.pep")
TOIG of: ag2934 check: 9987 from: 1 to: 385

P1:AG2934 - beta-lactamase [imported] - Agrobacterium tumefaciens (strain C58,
Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002

C:Accession: AG2934

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen,
Y.; Woo, L.; Kitajima, J.P.; Okura, V.K.; Almeida Jr., N.F.; Zhou, Y.; Boye
Sr., D.; Chapman, P.; Clendenning, J.; Deatherage, G.; Gillet, W.; Grant, C.;
Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; Mclelland, E.; Palmieri, A.;
Raymond, C.; Rouse, G.; Saenphimachak, C.; Wu, Z.; Gordon, D.; Eissen, J.A.;
Paulsen, I.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.;
Gordon-Kamm, B.; Liao, L.; Kim, S.; Hendrick, C.; Zhao, Z.; Dolan, M.; Tingey,
S.V.; Tomb, J.; Gordon, M.P.; Olson, M.V.; Nester, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AG2934

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-385 <KUR>

A:Cross-references: GB:AE00689; PIDN:AL43893.1; PID:917741441; GSPDB:GN00187

A:Experimental source: strain C58 (Dupont)

A:Genetics:

A:Gene: ampc

A:Map position: linear chromosome

C:Superfamily: Escherichia coli beta-lactamase

AG2934 Length: 385 March 17, 2003 12:10 Type: P Check: 9987 ..
Found using 'KTXS' (swope073.key)

...

286 AMTQDMWEQYTHPAPLKTIRELNGALTKTPVSEISPPMKPRDVPINTGSTNGRGA
336

346 YVAFIPKEKIGIVILANKNYPNEERVSAAVETITALEKRAQ

1 match found in sequence:

b2838 ; TOIG of: b2838 check: 8215 from: 1 to: 277
(from "lacktxs_pir.pep")
TOIG of: b2838 check: 8215 from: 1 to: 277

P1:B2838 - conserved hypothetical protein XF0186 [imported] - Xylella
fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

C:Accession: B2838

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for
Nucleotide Sequencing and Analysis, Sao Paulo, Brazil.

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: AB2515; MUID:20365717; PMID:10910347

A:Note: For a complete list of authors see reference number A59328 below

A:Accession: B2838

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-277 <SIM>

A:Cross-references: GB:AE003872; GB:AE003849; NID:99104975; PIDN:AF82999.1;
GSPDB:GN00128; XFSC:XF0186

A:Experimental source: strain 9a5c

R.Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Asencio, M.; Alvarenga, R.; Alves, L.M.C.; Araya, J.E.; Baia, G.S.; Baptista, C.S.; Barros, M.H.; Bonaccorsi, E.D.; Bordin, S.; Bove, J.M.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carver, H.; Colauto, N.B.; Colombo, C.; Costa, F.F.; Costa, M.C.R.; Costa-Neto, C.M.; Coutinho, L.L.; Cristofani, M.; Dias-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohne, M.; Furlan, L.R.; Garnier, M.; Goldman, G.H.; Goldman, M.H.S.; Gomes, S.L.; Gruber, A.; Ho, P.L.; Hobeisel, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, F.; Lambais, M.R.; Leite, L.C.C.; Lemos, E.G.M.; Lemos, M.V.F.; Lopes, S.A.; Lopes, C.R.; Machado, J.A.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.L.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Monteiro-Vitorello, C.B.; Moon, D.H.; Nagai, M.A.; Nascimento, M.L.T.O.; Neto, L.E.S.; Nhani Jr., A.; Nobrega, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Paris, A.; Peixoto, B.R.; Pereira, G.A.G.; Pereira Jr., H.A.; Pesquero, J.B.; Quaggio, R.B.; Roberto, P.G.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Saneili, R.V.; Sawasaki, H.E.

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, J.F.; Silvestri, M.L.Z.; Siqueira, W.J.; de Souza, A.A.; de Souza, A.P.; Terenzi, M.F.; Trufi, D.; Tsai, S.M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zago, M.A.; Zatz, M.; Melands, J.; Setubal, J.C.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF0186

C:Superfamily: beta-lactamase regulatory protein; beta-lactamase regulatory protein homology

B82838 Length: 277 March 17, 2003 12:10 Type: P Check: 8215 ..
Found using 'KTXS' (swope073.key)

66 LGDLLQIIFHSHMAEGCAFETDVTATITDKMVRHRPHVFGDITVDGKTYSTHWEAT
116

126 KRQREAVNEODHSLAGISSGLPEWDLRALKLERATRAFGRQA

1 match found in sequence:
c97855 : TOIG of: c97855 check: 7816 from: 1 to: 100
(from "lacks_pir.pep")
TOIG of: c97855 check: 7816 from: 1 to: 100

P1:C97855 - beta-lactamase homolog RCL243 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: C97855
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Sanson, D.; Roux, V.; Cossart, P.; Weissenbach, J.; Claverie, J.M.; Raoult, D.
Science 293, 2093-2098, 2001
A>Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: C97855

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-100 <KUR>

A:Cross-references: GB:AE006914; PIDN:AAL03781.1; PID:g15620377; GSPDB:GN00173

C:Genetics:

A:Gene: RCL243

C97855 Length: 100 March 17, 2003 12:10 Type: P Check: 7816 ..

Found using 'KTXS' (swope073.key)

1 MPVSVQAQENFTKNILFIEDVDCMKRGTGSGNSKLSQDRYVYKDKRKIGMFIWLQKND
29 32

61 RTVEFVHFIEHNKNRYDSYAGOR

1 match found in sequence:
f83132 : TOIG of: f83132 check: 9146 from: 1 to: 397
(from "lacks_pir.pep")
TOIG of: f83132 check: 9146 from: 1 to: 397

P1:F83132 - beta-lactamase precursor PA4110 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: F83132

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltzy, L.; Tolentino, E.; Westbrook-Wedman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, R.M.; Smith, K.A.; Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Salier, M.H.; Hancock, R.E.W.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: F83132

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-397 <STO>

A:Cross-references: GB:AE004827; GB:AE004091; NID:g9950306; PIDN:AA07497.1; GSPDB:GN00131; PASP:PA4110

A:Experimental source: strain PA01

C:Genetics:

A:Gene: ampc; PA4110

C:Superfamily: Escherichia coli beta-lactamase

F83132 Length: 397 March 17, 2003 12:10 Type: P Check: 9146 ..
Found using 'KTXS' (swope073.key)

292 MTQGLGWEAYDWPISLKLQAGNSTPMALQPHRIARLPAPQALEGORLLNKTGSGNGFGA
342

352 YVAFVGRDLGLVILANRRYPNAERKIAVAILSLGLEDQGVPL

1 match found in sequence:
h95971 : TOIG of: h95971 check: 1703 from: 1 to: 396
(from "lacks_pir.pep")
TOIG of: h95971 check: 1703 from: 1 to: 396

P1:H95971 - probable beta-lactamase (EC 3.5.2.6) [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid psymb

C:Species: Sinorhizobium meliloti

C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001

C:Accession: H95971

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernandez-Lucas, I.; Becker, A.; Cowie, A.; Gouzy, J.; Golding, B.; Puhler, A.

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A>Title: The complete sequence of the 1,683-kb psymb megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.

A:Reference number: A95842; MUID:21396508; PMID:11481431


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A:Accession: H95971
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-396 <KUR>
A:Cross-references: GB:AL591985; PIDN:CAC49440.1; PID:q15140926; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.;
Barloy-Hubler, F.; Barnett, M.J.; Becker, A.; Boistard, P.; Bothe, G.; Boutry,
M.; Bower, L.; Buhmester, J.; Cadieu, E.; Capela, D.; Chain, P.; Cowie, A.;
Davis, R.W.; Dreano, S.; Federzoni, N.A.; Fisher, R.F.; Gloux, S.; Godrie, T.;
Goffeau, A.; Golding, B.; Gouzy, J.; Gurjal, M.; Hernandez-Lucas, I.; Hong, A.;
Huizar, L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kallman, S.; Keating, D.H.; Kiss, E.; Komp, C.;
Lelaurie, V.; Masuy, D.; Palm, C.; Peck, M.C.; Pohl, T.M.; Portetelle, D.;
Purnelle, B.; Ransperger, U.; Surzycki, R.; Thebaud, P.; Vandendol, M.;
Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.; Batut, J.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: ampc; SMD21600
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: hydrolase
H95971 Length: 396 March 17, 2003 12:10 Type: P Check: 1703 ..
Found using 'KTXS' (swope073.key)

291 MTQGLGEMVPPYPTKIDLLAGNSSHMLPHKRVSKVPPAPQENLWIKGSGNGFGA
1--1
341
351 YAFVPAERIGIVLANKNYPPIPARVKAAYQILSTLESGSGSAD
1--1
1 match found in sequence:
H98347 : TOIG of: h98347 check: 8809 from: 1 to: 424
(from "lactxs_pir.pep")
TOIG of: h98347 check: 8809 from: 1 to: 424
P1:H98347 - ampc cephalosporinase precursor protein acc-1b (AF180955)
[Imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: H98347
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.;
Goldman, B.S.; Cao, Y.; Askew, M.; Halling, C.; Mullin, L.; Hounmel, K.;
Gordon, J.; Vaudin, M.; Iartchouk, O.; Epp, A.; Liu, F.; Wollam, C.; Allinger,
M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Flanagan, C.; Crowell, C.;
Gurson, J.; Lomo, C.; Sear, C.; Strub, G.; Cielo, C.; Slater, S.
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent
Agrobacterium tumefaciens C58.
A:Reference number: A97359; PMID:11743194
A:Accession: H98347
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-424 <KUR>
A:Cross-references: GB:AEO07870; PIDN:AAK90306.1; PID:q15160335; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L3464
A:Map position: linear chromosome
C:Superfamily: Escherichia coli beta-lactamase
H98347 Length: 424 March 17, 2003 12:10 Type: P Check: 8809 ..
Found using 'KTXS' (swope073.key)

```

```

325 AMTQDMVWEQYTHAPDKLTREINGALLKTVPSVSEISPPMKPREDFVINKTSGNGFGA
1--1
375
385 YAFIPKEXLGIIVLANKNYPNERVSAYEILLALEKAO
1--1
2 matches found in sequence:
139695 : TOIG of: 139695 check: 451 from: 1 to: 382
(from "lactxs_pir.pep")
TOIG of: 139695 check: 451 from: 1 to: 382
P1:139695 - beta-lactamase (EC 3.5.2.6) - Aeromonas sobria
C:Species: Aeromonas sobria
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-2002
C:Accession: 139695
R:Rasmussen, B.A.; Keeney, D.; Yang, Y.; Bush, K.
Antimicrob. Agents Chemother. 38, 2078-2085, 1994
A:Title: Cloning and expression of a cloxacillin-hydrolyzing enzyme and a
cephalosporinase from Aeromonas sobria ABR 14M in Escherichia coli: requirement
for an E. coli chromosomal mutation for efficient expression of the class D
enzyme.
A:Reference number: 139695; MUID:95110071; PMID:7811022
A:Accession: 139695
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-382 <RES>
A:Cross-references: EMBL:U01250; NID:9606838; PIDN:AAA83416.1; PID:9606839
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: hydrolase
139695 Length: 382 March 17, 2003 12:10 Type: P Check: 451 ..
Found using 'KTXS' (swope073.key)

196 SQTLLPGALLPTPSRCLRGMDYAGCAKEKPIRVNPGVLADENAVGKTSADLLAF
1--1
246
256 VKANISGVDRALQQAISLTHQGRYSVGEMTQGLWESYAVPSEQTLLAGNSSAVIYA
1--1
316 NPVKFPAASQETGARLYNKKGSTNGEGAYAFPAKIGIVLANKNYPPIPARVKAAYA
335
376 ILSKLIAD
1--1
1 match found in sequence:
140198 : TOIG of: 140198 check: 299 from: 1 to: 582
(from "lactxs_pir.pep")
TOIG of: 140198 check: 299 from: 1 to: 582
P1:140198 - transposase - Bacteroides fragilis
C:Species: Bacteroides fragilis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 08-Oct-1999
C:Accession: 140198
R:Rogers, M.B.; Bennett, T.K.; Payne, C.M.; Smith, C.J.
J. Bacteriol. 176, 4376-4384, 1994
A:Title: Insertional activation of cepA leads to high-level beta-lactamase
expression in Bacteroides fragilis clinical isolates.
A:Reference number: 140192; MUID:94292468; PMID:7517394
A:Accession: 140198
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-582 <RES>
A:Cross-references: EMBL:U05888; NID:9458311; PIDN:AAA21540.1; PID:9458314
C:Genetics:
A:Gene: tnpA
140198 Length: 582 March 17, 2003 12:10 Type: P Check: 299 ..

```

Found using 'KTXS' (swope073.key)

1 MIHGHILLILDRPHLFHRIVDNFTSGKESRSMHFYRGMIPLPGSNVYLCLNKETD
30 33

61 TGMETKSONLKDKLMMYKYREL

1 match found in sequence:
140231 ; TOIG of: 140231 check: 1067 from: 1 to: 296
(from "lacks_pir.pep")
TOIG of: 140231 check: 1067 from: 1 to: 296

PI:140231 - beta-lactamase - Bacteroides uniformis

C:Species: Bacteroides uniformis

C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 29-Sep-1999

C:Accession: 140231

R:Smith, C.J.; Bennett, T.K.; Parker, A.C.

Antimicrob. Agents Chemother. 38, 1711-1715, 1994

A:Title: Molecular and genetic analysis of the Bacteroides uniformis

cephalosporinase gene, cblA, encoding the species-specific beta-lactamase.

A:Reference number: 140230; MUID:95077321; PMID:7985999

A:Accession: 140231

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-296 <RES>

A:Cross-references: GB:L08472; NID:g436817; PIDN:AAA6962.1; PID:g143930

A:Gene: cblA

C:Genetics:

C:Superfamily: Pseudomonas aeruginosa beta-lactamase

140231 Length: 296 March 17, 2003 12:10 Type: P Check: 1067 ..
Found using 'KTXS' (swope073.key)

185 AMVRLFTADEKELFSNKEKLDLMQMTIDETGANKLKGMLEPAKTVYGGKTSRDNAD
235

245 GMRADNDAGLVITPDGRKYIAFAVWDSYEDDNANITARIIS

1 match found in sequence:

jl0091 ; TOIG of: jl0091 check: 6233 from: 1 to: 310

(from "lacks_pir.pep")

TOIG of: jl0091 check: 6233 from: 1 to: 310

PI:jl0091 - beta-lactamase (EC 3.5.2.6) precursor - Bacillus sp. (strain 170)

N:Alternate names: lipo-penicillinase

C:Species: Bacillus sp.

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Jun-2000

C:Accession: jl0091

R:Kato, C.; Nakano, Y.; Horikoshi, K.

Arch. Microbiol. 151, 91-94, 1989

A:Title: The nucleotide sequence of the lipo-penicillinase gene of alkalophilic

Bacillus sp. strain 170.

A:Reference number: jl0091; MUID:89245965; PMID:2655551

A:Accession: jl0091

A:Molecule type: mRNA

A:Residues: 1-310 <KAT>

A:Cross-references: GB:D10848; NID:g216225; PIDN:BA01621.1; PID:g216226

C:Superfamily: beta-lactamase I

C:Keywords: hydrolase; lipoprotein

F:1-29/Domain: signal sequence #status predicted <STG>

F:30-310/Product: beta-lactamase #status predicted <KAT>

F:89/Active site: Ser #status predicted

jl0091 Length: 310 March 17, 2003 12:10 Type: P Check: 6233 ..
Found using 'KTXS' (swope073.key)

...

201 KALATSLQAVALGDILSVENRNLIDLMKRTTGDNLIRAGVGEVEVDDTGSQSYCTR
251

261 NDIAFIWPPNKKPFILAILISNOAKEDAKYDOKLIDAKTIVLDV

1 match found in sequence:
jp0074 ; TOIG of: jp0074 check: 8145 from: 1 to: 291
(from "lacks_pir.pep")
TOIG of: jp0074 check: 8145 from: 1 to: 291

PI:jp0074 - beta-lactamase (EC 3.5.2.6), cefotaxime-hydrolyzing - Escherichia

coli

C:Species: Escherichia coli

C>Date: 22-Apr-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jul-2000

C:Accession: jp0074; 141146

R:ishii, Y.; Ohno, A.; Taguchi, H.; Imajo, S.; Ishiguro, M.; Matsuzawa, H.

submitted to JIPID, July 1995

A:Description: Cloning and the sequence analysis of a cefotaxime-hydrolyzing

Class A beta-lactamase gene isolate from Escherichia coli.

A:Reference number: JP0074

A:Accession: jp0074

A:Molecule type: protein

A:Residues: 1-291 <ISH>

R:ishii, Y.; Ohno, A.; Taguchi, H.; Matsuzawa, H.; Yamaguchi, K.

Antimicrob. Agents Chemother. 39, 2269-2275, 1995

A:Title: Cloning and sequence analysis of the gene for a cefotaxime-hydrolyzing

Class A beta-lactamase from Escherichia coli.

A:Reference number: 141146; MUID:96109425; PMID:8619581

A:Accession: 141146

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-89, 'D', '91-291 <RES>

A:Cross-references: GB:D37830; NID:g1435024; PIDN:BA07082.1; PID:g1037162

C:Superfamily: beta-lactamase I

C:Keywords: hydrolase

jp0074 Length: 291 March 17, 2003 12:10 Type: P Check: 8145 ..
Found using 'KTXS' (swope073.key)

187 LAMAQTLNKLNLGKALAFQRAQLVTWLKGNVTGSASTRAGLPKSWVVGKTSGDYGT
237

247 NDIAVWPNHAPLVLTFTYTPQPKAKERRRDIILAAAKIVTHG

1 match found in sequence:

pnkkm ; TOIG of: pnkkm check: 1311 from: 1 to: 381

(from "lacks_pir.pep")

TOIG of: pnkkm check: 1311 from: 1 to: 381

PI:PNKBM - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain

MNH1)

N:Alternate names: cephalosporinase

C:Species: Enterobacter cloacae

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 30-Jun-1993

C:Accession: S00406

R:Galleni, M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;

Freire, J.M.

Biochem. J. 250, 753-760, 1988

```

A:Title: Sequence and comparative analysis of three Enterobacter cloacae ampC
beta-lactamase genes and their products.
A:Reference number: S00404; MUID:88268750; PMID:3260487
A:Accession: S00406
A:Molecule type: DNA
A:Residues: 1-381 <GAL>
A:Cross-references: EMBL:X08082
C:Comment: This protein is a class C beta-lactamase.
C:Genetics:
A:Gene: ampC
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-381/Product: beta-lactamase #status predicted <MAT>
F:84/Active site: Ser #status predicted

PNKBP Length: 381 March 17, 2003 12:10 Type: P Check: 1311 ..
Found using 'KTXS' (swpo073.key)

...

285 MYOGLGEMLMNPVEANTVVEGSDSKVALAPLPVAEVPNPAPPVKASWVKHGSGTGGFGS
335

1--1
1 match found in sequence:
pnkbp ; TOIG of: pnkbp check: 735 from: 1 to: 381
(from "lactkxs_dir.pep")
TOIG of: pnkbp check: 735 from: 1 to: 381

p99)
P1:PNKBP - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain
N)Alternate names: cephalosporinase
C:Species: Enterobacter cloacae
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Jun-1999
C:Accession: S00404
R:Galleni,M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;
Frere,J.M.
Biochem. J. 250, 753-760, 1988
A:Title: Sequence and comparative analysis of three Enterobacter cloacae ampC
beta-lactamase genes and their products.
A:Reference number: S00404; MUID:88268750; PMID:3260487
A:Accession: S00404
A:Molecule type: DNA
A:Residues: 1-381 <GAL>
A:Cross-references: EMBL:X07274; NID:g42260; PID:CAA30257.1; PID:g42261
A:Note: part of this sequence, including the carboxyl end of the mature
protein, was confirmed by protein sequencing
C:Comment: This protein is a class C beta-lactamase.
C:Genetics:
A:Gene: ampC
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-381/Product: beta-lactamase #status experimental <MAT>
F:84/Active site: Ser #status predicted

PNKBP Length: 381 March 17, 2003 12:10 Type: P Check: 735 ..
Found using 'KTXS' (swpo073.key)

...

345 YVAFPEKQIGIVMLANKSYNPAPVAAVHILEAQ
335

1--1
1 match found in sequence:
pnkbp ; TOIG of: pnkbp check: 735 from: 1 to: 381
(from "lactkxs_dir.pep")
TOIG of: pnkbp check: 735 from: 1 to: 381

p99)
P1:PNKBP - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain
N)Alternate names: cephalosporinase
C:Species: Enterobacter cloacae
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Jun-1999
C:Accession: S00404
R:Galleni,M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;
Frere,J.M.
Biochem. J. 250, 753-760, 1988
A:Title: Sequence and comparative analysis of three Enterobacter cloacae ampC
beta-lactamase genes and their products.
A:Reference number: S00404; MUID:88268750; PMID:3260487
A:Accession: S00404
A:Molecule type: DNA
A:Residues: 1-381 <GAL>
A:Cross-references: EMBL:X07274; NID:g42260; PID:CAA30257.1; PID:g42261
A:Note: part of this sequence, including the carboxyl end of the mature
protein, was confirmed by protein sequencing
C:Comment: This protein is a class C beta-lactamase.
C:Genetics:
A:Gene: ampC
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-381/Product: beta-lactamase #status experimental <MAT>
F:84/Active site: Ser #status predicted

PNKBP Length: 381 March 17, 2003 12:10 Type: P Check: 735 ..
Found using 'KTXS' (swpo073.key)

...

285 MYOGLGEMLMNPVEANTVVEGSDSKVALAPLPVAEVPNPAPPVKASWVKHGSGTGGFGS
335

1--1
1 match found in sequence:
pnkbp ; TOIG of: pnkbp check: 735 from: 1 to: 381
(from "lactkxs_dir.pep")
TOIG of: pnkbp check: 735 from: 1 to: 381

p99)
P1:PNKBP - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain
N)Alternate names: cephalosporinase
C:Species: Enterobacter cloacae
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Jun-1999
C:Accession: S00404
R:Galleni,M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;
Frere,J.M.
Biochem. J. 250, 753-760, 1988
A:Title: Sequence and comparative analysis of three Enterobacter cloacae ampC
beta-lactamase genes and their products.
A:Reference number: S00404; MUID:88268750; PMID:3260487
A:Accession: S00404
A:Molecule type: DNA
A:Residues: 1-381 <GAL>
A:Cross-references: EMBL:X07274; NID:g42260; PID:CAA30257.1; PID:g42261
A:Note: part of this sequence, including the carboxyl end of the mature
protein, was confirmed by protein sequencing
C:Comment: This protein is a class C beta-lactamase.
C:Genetics:
A:Gene: ampC
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-381/Product: beta-lactamase #status experimental <MAT>
F:84/Active site: Ser #status predicted

PNKBP Length: 381 March 17, 2003 12:10 Type: P Check: 735 ..
Found using 'KTXS' (swpo073.key)

...

345 YVAFPEKQIGIVMLANKSYNPAPVAAVHILEAQ
335

1--1
1 match found in sequence:
pnkbp ; TOIG of: pnkbp check: 735 from: 1 to: 381
(from "lactkxs_dir.pep")
TOIG of: pnkbp check: 735 from: 1 to: 381

p99)
P1:PNKBP - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain
N)Alternate names: cephalosporinase
C:Species: Enterobacter cloacae
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Jun-1999
C:Accession: S00404
R:Galleni,M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;
Frere,J.M.
Biochem. J. 250, 753-760, 1988
A:Title: Sequence and comparative analysis of three Enterobacter cloacae ampC
beta-lactamase genes and their products.
A:Reference number: S00404; MUID:88268750; PMID:3260487
A:Accession: S00404
A:Molecule type: DNA
A:Residues: 1-381 <GAL>
A:Cross-references: EMBL:X07274; NID:g42260; PID:CAA30257.1; PID:g42261
A:Note: part of this sequence, including the carboxyl end of the mature
protein, was confirmed by protein sequencing
C:Comment: This protein is a class C beta-lactamase.
C:Genetics:
A:Gene: ampC
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-381/Product: beta-lactamase #status experimental <MAT>
F:84/Active site: Ser #status predicted

PNKBP Length: 381 March 17, 2003 12:10 Type: P Check: 735 ..
Found using 'KTXS' (swpo073.key)

...

285 MYOGLGEMLMNPVEANTVVEGSDSKVALAPLPVAEVPNPAPPVKASWVKHGSGTGGFGS
335

1--1
1 match found in sequence:
pnkbp ; TOIG of: pnkbp check: 735 from: 1 to: 381
(from "lactkxs_dir.pep")
TOIG of: pnkbp check: 735 from: 1 to: 381

p99)
P1:PNKBP - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain
N)Alternate names: cephalosporinase
C:Species: Enterobacter cloacae
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Jun-1999
C:Accession: S00404
R:Galleni,M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;
Frere,J.M.
Biochem. J. 250, 753-760, 1988
A:Title: Sequence and comparative analysis of three Enterobacter cloacae ampC
beta-lactamase genes and their products.
A:Reference number: S00404; MUID:88268750; PMID:3260487
A:Accession: S00404
A:Molecule type: DNA
A:Residues: 1-381 <GAL>
A:Cross-references: EMBL:X07274; NID:g42260; PID:CAA30257.1; PID:g42261
A:Note: part of this sequence, including the carboxyl end of the mature
protein, was confirmed by protein sequencing
C:Comment: This protein is a class C beta-lactamase.
C:Genetics:
A:Gene: ampC
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-381/Product: beta-lactamase #status experimental <MAT>
F:84/Active site: Ser #status predicted

PNKBP Length: 381 March 17, 2003 12:10 Type: P Check: 735 ..
Found using 'KTXS' (swpo073.key)

...

345 YVAFPEKQIGIVMLANKSYNPAPVAAVHILEAQ
335

1--1
1 match found in sequence:
pnkbp ; TOIG of: pnkbp check: 735 from: 1 to: 381
(from "lactkxs_dir.pep")
TOIG of: pnkbp check: 735 from: 1 to: 381

p99)
P1:PNKBP - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain
N)Alternate names: cephalosporinase
C:Species: Enterobacter cloacae
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Jun-1999
C:Accession: S00404
R:Galleni,M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;
Frere,J.M.
Biochem. J. 250, 753-760, 1988
A:Title: Sequence and comparative analysis of three Enterobacter cloacae ampC
beta-lactamase genes and their products.
A:Reference number: S00404; MUID:88268750; PMID:3260487
A:Accession: S00404
A:Molecule type: DNA
A:Residues: 1-381 <GAL>
A:Cross-references: EMBL:X07274; NID:g42260; PID:CAA30257.1; PID:g42261
A:Note: part of this sequence, including the carboxyl end of the mature
protein, was confirmed by protein sequencing
C:Comment: This protein is a class C beta-lactamase.
C:Genetics:
A:Gene: ampC
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-381/Product: beta-lactamase #status experimental <MAT>
F:84/Active site: Ser #status predicted

PNKBP Length: 381 March 17, 2003 12:10 Type: P Check: 735 ..
Found using 'KTXS' (swpo073.key)

...

285 MYOGLGEMLMNPVEANTVVEGSDSKVALAPLPVAEVPNPAPPVKASWVKHGSGTGGFGS
335

1--1
1 match
```

F1:PNKBO - beta-lactamase (EC 3.5.2.6) precursor - Enterobacter cloacae (strain
 0908R) (fragment)
 N:Alternate names: cephalosporinase
 C:Species: Enterobacter cloacae
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Jun-1999
 C:Accession: S00405
 R:Gallenl, M.; Lindberg, F.; Normark, S.; Cole, S.; Honore, N.; Joris, B.;
 Frere, J.M.
 Biochem. J. 250, 753-760, 1988
 A:Title: Sequence and comparative analysis of three Enterobacter cloacae ampC
 beta-lactamase genes and their products.
 A:Reference number: S00404; MID:88268750; PMID:3260487
 A:Accession: S00405
 A:Molecule type: DNA
 A:Residues: 1-375 <GAL>
 A:Cross-references: EMBL:X08081; NID:g42611; PIDN:CAA30878.1; PID:g757841
 A:Note: parts of this sequence, including the amino and carboxyl ends of the
 mature protein, were confirmed by protein sequencing
 C:Comment: This protein is a class C beta-lactamase.
 C:Genetics:
 A:Gene: ampC
 C:Superfamily: Escherichia coli beta-lactamase
 C:Keywords: antibiotic resistance; hydrolase
 F:1-14/Domain1: signal sequence (fragment) #status predicted <SIG>
 F:15-375/Product: beta-lactamase #status experimental <MAT>
 F:78/Active site: Ser #status predicted

 PNKBO Length: 375 March 17, 2003 12:10 Type: P Check: 9705 ..
 Found using 'KTXS' (swpe073.key)

 279 MIOGLCEMLNPNVEANTYVEGSDSKVALAPRYVEVNPAPRYKASWYHKTSIGFGCS
 329
 339 YVAFIPEKQIGIYMLANTSYNPAPRYEAYHILEALO
 1--1
 1 match found in sequence:
 pnsmlu ; TOIG of: pnsmlu check: 9207 from: 1 to: 314
 (from "lactlxs_pir.pep")
 TOIG of: pnsmlu check: 9207 from: 1 to: 314

 P1:PNSM1U - beta-lactamase (EC 3.5.2.6) precursor - Streptomyces albus
 N:Alternate names: penicillinase
 C:Species: Streptomyces albus
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
 C:Accession: S00057; S18494; S01468
 R:Dehottay, P.; Dusart, J.; de Weester, F.; Joris, B.; van Beeumen, J.;
 Eripcium, T.; Frere, J.M.; Ghuyssen, J.M.
 Eur. J. Biochem. 160, 345-350, 1987
 A:Title: Nucleotide sequence of the gene encoding the Streptomyces albus G
 beta-lactamase precursor.
 A:Reference number: S00057; MID:87275916; PMID:3038538
 A:Accession: S00057
 A:Molecule type: DNA
 A:Residues: 1-314 <DEH>
 A:Cross-references: EMBL:M28303; NID:g153338; PIDN:AAA26775.1; PID:g153339
 A:Experimental source: strain G; plasmid pMML6
 A:Note: the authors translated the initiation codon GTG for residue 1 as Val
 A:Accession: S18494
 A:Molecule type: protein
 A:Residues: 40-55;187-209 <DEH2>
 R:de Weester, F.; Joris, B.; Lenzini, M.V.; Dehottay, P.; Eripcium, T.; Dusart,
 J.; Klein, D.; Ghuyssen, J.M.; Frere, J.M.; van Beeumen, J.
 Biochem. J. 244, 427-432, 1987
 A:Title: The active sites of the beta-lactamases of Streptomyces cacaoi and
 Streptomyces albus G.

```

A:Reference number: S01468; MUID:88024011; PMID:2822004
A:Accession: S01468
A:Molecule type: protein
A:Residues: 81-92 <DEM>
A:Experimental source: strain G; cloned gene from plasmid pDM16 overexpressed
  in Streptomyces lividans
C:Comment: This is a class A beta-lactamase.
C:Genetics:
A:Start codon: GTG
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; extracellular protein; hydrolase
F:1-39/Domain: signal sequence #status predicted <SIG>
F:40-514/Product: beta-lactamase #status experimental <MAT>
F:89/Active site: Ser #status experimental

PNSM1U Length: 314 March 17, 2003 12:10 Type: P Check: 9207 ..
Found using 'KTXS' (swope073.key)

42 GSGVSDAERRLAGLERASGARLGYYAYDTGSGRTVAYRADELPMCSVFETLSSAVALR 1-1
62 95

102 DLDNRGEFLSRRLTYTQDDVEQADGAGPRTGKPNLANAQLTVE

-----
1 match found in sequence:
gkse : TOIG of: gkse check: 107 from: 1 to: 376
      (from "lacks_pir.pep")
TOIG of: gkse check: 107 from: 1 to: 376

P1:OKSE - beta-lactamase (EC 3.5.2.6) precursor - Serratia marcescens
C:Species: Serratia marcescens
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1999
C:Accession: A48176; S11710
R:Nomura, K.; Yoshida, T.
FMS Microbiol. Lett. 70, 295-300, 1990
A:Title: Nucleotide sequence of the Serratia marcescens SR50 chromosomal ampc
  beta-lactamase gene.
A:Reference number: A48176
A:Accession: A48176
A:Molecule type: DNA
A:Residues: 1-376 <NOM>
A:Cross-references: EMBL:X52964; NID:947223; PIDN:CAA37137.1; PID:947224
A:Note: submitted to the EMBL Data Library, May 1990
A:Note: the authors translated the codon GTA for residue 258 as Asp
C:Genetics:
A:Gene: ampc
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-376/Product: beta-lactamase #status predicted <MAT>
F:79/Active site: Ser #status predicted

OKSE Length: 376 March 17, 2003 12:10 Type: P Check: 107 ..
Found using 'KTXS' (swope073.key)

278 FTODLWENYRPVKLSRLIEGNNAGIMNGTPATATPPPELRAGMYNKGTSGTGFST 1-1
328

338 YAVFIKATIAVEMLANKMPNDRVEAAHHIIOALEKR

-----
1 match found in sequence:
s08296 : TOIG of: s08296 check: 580 from: 1 to: 381
      (from "lacks_pir.pep")
TOIG of: s08296 check: 580 from: 1 to: 381

P1:S08296 - beta-lactamase (EC 3.5.2.6) precursor - Citrobacter freundii
(strain GN346)
N:Alternate names: cephalosporinase
C:Species: Citrobacter freundii
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Oct-1999
C:Accession: S08296; A60909; A27028; A24869
R:Tsukamoto, K.; Tachibana, K.; Yamazaki, N.; Ishii, Y.; Ujile, K.; Nishida,
  N.; Sawai, T.
Eur. J. Biochem. 188, 15-22, 1990
A:Title: Role of lysine-67 in the active site of class C beta-lactamase from
  Citrobacter freundii GN346.
A:Reference number: S08296; MUID:90201023; PMID:1969344
A:Accession: S08296
A:Molecule type: DNA
A:Residues: 1-381 <TSU>
A:Cross-references: GB:X51632; NID:940457; PIDN:CAA35959.1; PID:940458
A:Note: part of this sequence was confirmed by amino acid sequencing
  R:Sawai, T.; Yamaguchi, A.; Tsukamoto, K.
  Rev. Infect. Dis. 10, 721-725, 1988
A:Title: Amino acid sequence, active-site residue, and effect of suicide
  inhibitors on cephalosporinase of Citrobacter freundii GN346.
A:Reference number: A60909; MUID:89043488; PMID:3263684
A:Accession: A60909
A>Status: nucleic acid sequence not shown; not compared with conceptual
  translation
A:Molecule type: DNA
A:Residues: 21-97, 'T', '99-381 <SAW>
R:Yamaguchi, A.; Adachi, H.; Sawai, T.
FEBS Lett. 218, 126-130, 1987
A:Title: Identification of the active site of Citrobacter freundii
  beta-lactamase using dansyl-penicillin.
A:Reference number: A27028; MUID:87247241; PMID:3496243
A:Accession: A27028
A:Molecule type: protein
A:Residues: 66-87 <YAM>
R:Lindberg, F.; Normark, S.
Eur. J. Biochem. 156, 441-445, 1986
A:Title: Sequence of the Citrobacter freundii OS60 chromosomal ampc
  beta-lactamase gene.
A:Reference number: A24869; MUID:86192473; PMID:3486121
A:Accession: A24869
A:Molecule type: DNA
A:Residues:
  1-96, 'R', '98-142, 'G', '144, 'V', '146-149, 'E', '151-184, 'S', '186-223, 'L', '225-242, 'V', '244-
  324, 'A', '326-367, 'A', '369-381 <LIN>
A:Cross-references: GB:X03866; NID:940451; PIDN:CAA27494.1; PID:940452
A:Experimental source: wild-type isolate OS60
C:Genetics:
A:Gene: ampc
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: antibiotic resistance; hydrolase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-381/Product: beta-lactamase #status predicted <MAT>
F:84,87/Active site: Ser, Lys #status experimental

S08296 Length: 381 March 17, 2003 12:10 Type: P Check: 580 ..
Found using 'KTXS' (swope073.key)

285 MYOGLGEMLNMPKADSIINGSDSKVALALPAVEVNPVPVAKASWVHKGTSGTGFSGS 1-1
335

345 YVAFVPERNLGIYMLANKSYRNPVVEAAMRIELKQ

-----
1 match found in sequence:
s13408 : TOIG of: s13408 check: 8211 from: 1 to: 397
      (from "lacks_pir.pep")
TOIG of: s13408 check: 8211 from: 1 to: 397

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P1:S13408 - beta-lactamase (EC 3.5.2.6) precursor - *Pseudomonas aeruginosa*
 C:Species: *Pseudomonas aeruginosa*
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 22-Jun-1999
 C:Accession: S13408
 R:Blodgett, J.M.; Minchin, S.D.; Piddock, L.J.V.; Busby, S.J.W.
 Biochem. J. 272, 627-631, 1990
 A>Title: Cloning, sequencing and analysis of the structural gene and regulatory region of the *Pseudomonas aeruginosa* chromosomal amp^c beta-lactamase.
 A:Reference number: S13407; MUID:91097488; PMID:2125210
 A:Accession: S13408
 A:Molecule type: DNA
 A:Residues: 1-397 <LDB>
 A:Cross-references: EMBL:X54719; NID:945272; PIDN:CAA38522.1; PID:945273
 A>Note: the authors translated the codon GAC for residue 76 as Asn
 C:Genetics:
 A:Gene: amp^c
 C:Superfamily: *Escherichia coli* beta-lactamase
 C:Keywords: antibiotic resistance; hydrolase
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-397/Product: beta-lactamase #status predicted <MAT>

S13408 Length: 397 March 17, 2003 12:10 Type: P Check: 8211 ..
 Found using 'KTXS' (swope073.key)

292 MTGIGWEAYMPISLKLQAGNSTPMALQPHRIARLPAPALBESORLNTKGTSTNGCA
 342

352 YVAFVGRDLGLVILANRNPNAERVKIAYAILSGLEQGRKVP

1 match found in sequence:
 S16553 ; TOIG of: S16553 check: 2339 from: 1 to: 294
 (from "lactxs.pir.pep")
 TOIG of: S16553 check: 2339 from: 1 to: 294

P1:S16553 - beta-lactamase (EC 3.5.2.6) - *Yersinia enterocolitica*
 C:Species: *Yersinia enterocolitica*
 C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S16553
 R:Seoane, A.; Garcia Lobo, J.M.
 Mol. Gen. Genet. 228, 215-220, 1991
 A>Title: Nucleotide sequence of a new class A beta-lactamase gene from the chromosome of *Yersinia enterocolitica*: implications for the evolution of class A beta-lactamases.
 A:Reference number: S16552; MUID:91360067; PMID:1886608
 A:Accession: S16553
 A:Molecule type: DNA
 A:Residues: 1-294 <SEO>
 A:Cross-references: EMBL:X57074; NID:948813; PIDN:CAA40357.1; PID:948814
 C:Superfamily: beta-lactamase I
 C:Keywords: hydrolase
 S16553 Length: 294 March 17, 2003 12:10 Type: P Check: 2339 ..
 Found using 'KTXS' (swope073.key)

189 AAMASMKIVLGDALRPAQSQSLAVMLKGNFTGDATTAGAPDMIVGDDTSGSDYGT
 239

249 NDIAVIMPTKAPIVLVYFTQREKDAKPRRDVLAIVTKIILSQ

1 match found in sequence:
 S23929 ; TOIG of: S23929 check: 1881 from: 1 to: 263

(from "lactxs.pir.pep")
 TOIG of: S23929 check: 1881 from: 1 to: 263
 P1:S23929 - beta-lactamase (EC 3.5.2.6) - *Klebsiella oxytoca*
 C:Species: *Klebsiella oxytoca*
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
 C:Accession: S23929
 R:Barthelemy, M.; Peduzzi, J.; Bernard, H.; Tancrède, C.; Labie, R.
 Biochim. Biophys. Acta 1122, 15-22, 1992
 A>Title: Close amino acid sequence relationship between the new plasmid-mediated extended-spectrum beta-lactamase MEN-1 and chromosomally encoded enzymes of *Klebsiella oxytoca*.
 A:Reference number: S23929; MUID:92338218; PMID:1633193
 A:Accession: S23929
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-263 <BAR>
 C:Superfamily: beta-lactamase I
 C:Keywords: hydrolase
 S23929 Length: 263 March 17, 2003 12:10 Type: P Check: 1881 ..
 Found using 'KTXS' (swope073.key)

159 RAMAQIRNLTLKALGDSQRAQVYTMKGNITGASIQAGLPASWVYGDKSGDYGTT
 209

219 NDIAVIMPTKAPIVLVYFTQREKDAKPRRDVLAIVTKIILSQ

2 matches found in sequence:
 S27528 ; TOIG of: S27528 check: 4541 from: 1 to: 321
 (from "lactxs.pir.pep")
 TOIG of: S27528 check: 4541 from: 1 to: 321

P1:S27528 - beta-lactamase (EC 3.5.2.6) cfxA precursor - *Bacteroides vulgatus*
 C:Species: *Bacteroides vulgatus*
 C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 29-Sep-1999
 C:Accession: I40600; S27528; S70948; S70951
 R:Parker, A.C.; Smith, C.J.
 Antimicrob. Agents Chemother. 37, 1028-1036, 1993
 A>Title: Genetic and biochemical analysis of a novel Ambler class A beta-lactamase responsible for cefoxitin resistance in *Bacteroides* species.
 A:Reference number: I40600; MUID:93297917; PMID:8517690
 A:Accession: I40600
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-321 <RES>
 A:Cross-references: EMBL:U38243; NID:91079657; PIDN:AAB17891.1; PID:91079658
 R:Smith, C.J.; Parker, A.C.
 Mol. Microbiol. 20, 741-750, 1996
 A>Title: A gene product related to Tral is required for the mobilization of *Bacteroides* mobilizable transposons and plasmids
 A:Reference number: S70948; MUID:96386042; PMID:8793871
 A:Contents: annotation; transposon
 C:Genetics:
 A:Gene: cfxA
 A:Mobile element: transposon Tn4555
 C:Superfamily: *Pseudomonas aeruginosa* beta-lactamase
 C:Keywords: antibiotic resistance; hydrolase
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-321/Product: beta-lactamase cfxA #status predicted <MAT>
 S27528 Length: 321 March 17, 2003 12:10 Type: P Check: 4541 ..
 Found using 'KTXS' (swope073.key)

```

68      RDTVKNKSVYPMMSVEKQALALCNDPDKGISLDTLVNINRDKLPKTSPEMLKDY      |--|
      118
128      SGPVISTVRLRLRYTLTQSDNNNSNLKFKDMVNVVAQTDSFIAT
      ...
204      AAMLMNRLFTGCLIDDEKQSFIKNTLKCKCTGVDRIRIAPLLDKGCVIAHKTSQGYVNNEN      |--|
      254
264      GVLAANDVAYICLPNNISYTLAVFVKDKGKNSQASQYAHIS
      ...
-----
1 match found in sequence:
s35915 ; TOIG of: s35915 check: 472 from: 1 to: 292
(from "lactxs_pir.pep")
TOIG of: s35915 check: 472 from: 1 to: 292

P1:S35915 - beta-lactamase (EC 3.5.2.6) - Enterobacter cloacae
C:Species: Enterobacter cloacae
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S35915
R:Naas, T.; Nordmann, P.; Mariotte, S.; Arber, W.
submitted to the EMBL Data Library, March 1993
A:Description: A carbapenem-hydrolysing beta-lactamase from Enterobacter
cloacae NOR-1: Sequence analysis and regulation.
A:Reference number: S35914
A:Accession: S35915
A:Molecule type: DNA
A:Residues: 1-292 <NAA>
A:Cross-references: EMBL:Z21956; NID:9396086; PIDN:CAA7967.1; PID:9396088
C:Superfamily: beta-lactamase I
C:Keywords: hydrolase

S35915 Length: 292 March 17, 2003 12:10 Type: P Check: 472 ..
Found using 'KTXS' (swope073.key)

...
186      AAVAKSLKTLALGNLSEHEKETQYWLKNTGAGARIRASVPSDWWGDKTSGCAYGT      |--|
      236
246      ANDYAVVWPKNRAPLIISVYTTKNEKAKHEDKVIAEHSRIAID
      ...
-----
1 match found in sequence:
s36188 ; TOIG of: s36188 check: 8442 from: 1 to: 302
(from "lactxs_pir.pep")
TOIG of: s36188 check: 8442 from: 1 to: 302

P1:S36188 - beta-lactamase (EC 3.5.2.6) I precursor - Streptomyces lactamdurans
C:Species: Streptomyces lactamdurans
C>Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 22-Jun-1999
C:Accession: S36188; S22750
R:Coque, J.J.R.; Liras, P.; Martin, J.F.
EMBO J. 12, 631-639, 1993
A>Title: Genes for a beta-lactamase, a penicillin-binding protein and a
transmembrane protein are clustered with the cephamycin biosynthetic genes in
Nocardia lactamdurans.
A:Reference number: S36188; MUID:93178438; PMID:8440253
A:Accession: S36188
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-302 <COO>
A:Cross-references: EMBL:Z13971; NID:944996; PIDN:CAA78373.1; PID:9581412
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June

```

```

1992
C:Genetics:
A:Gene: bla
A:Start codon: GTG
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase; penicillin resistance
F:1-29/Domain: signal sequence #status predicted <Sig>
F:30-302/Product: beta-lactamase I #status predicted <Mat>
F:85/Active site: Ser #status predicted

S36188 Length: 302 March 17, 2003 12:10 Type: P Check: 8442 ..
Found using 'KTXS' (swope073.key)

...
197      RALAHDLRFVLGDLALAEDDRALLTDLRLNRTTGTIVRAGVPADWYVDKRTSGSYGGR      |--|
      247
257      NDYAVLMPNRPAPIVMAVMTSREPRKRRADLLADAAVAVTA
      ...
-----
1 match found in sequence:
s39196 ; TOIG of: s39196 check: 861 from: 1 to: 381
(from "lactxs_pir.pep")
TOIG of: s39196 check: 861 from: 1 to: 381

P1:S39196 - beta-lactamase (EC 3.5.2.6) - Escherichia coli
C:Species: Escherichia coli
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S39196
R:Posberry, A.; Payne, D.J.; Lawlor, E.J.; Hodgson, J.E.
submitted to the EMBL Data Library, September 1993
A:Description: Cloning and sequence analysis of bla BIL-1: a plasmid mediated
class C beta-lactamase gene in Escherichia coli BS.
A:Reference number: S39196
A:Accession: S39196
A:Molecule type: DNA
A:Residues: 1-381 <POS>
A:Cross-references: EMBL:X74512; NID:9433560; PIDN:CAA52618.1; PID:9433561
C:Superfamily: Escherichia coli beta-lactamase
C:Keywords: hydrolase
F:84/Active site: Ser #status predicted

S39196 Length: 381 March 17, 2003 12:10 Type: P Check: 861 ..
Found using 'KTXS' (swope073.key)

...
285      MIOGLGEMLMNPLKADSIINSQDKVALAAYPAVEVNPAPAVKASVHKTGSGGSGS      |--|
      335
345      YVAFVEKNLGIYIVANKSYPNPVRVEAARILKIQ
      ...
-----
2 matches found in sequence:
s41941 ; TOIG of: s41941 check: 7779 from: 1 to: 382
(from "lactxs_pir.pep")
TOIG of: s41941 check: 7779 from: 1 to: 382

P1:S41941 - beta-lactamase, class C - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Jun-1999
C:Accession: S41941
R:Gonzalez-Ieliza, M.; Perez-Diaz, J.C.; Casellas, J.M.; Martinez-Beltran, J.;
Bush, K.; Baquero, F.
submitted to the EMBL Data Library, January 1994
A:Description: Gene sequence and biochemical characterization of FOX-1 from
Klebsiella pneumoniae a new ampc-plasmid mediated beta-lactamase with two
molecular variants.

```

A:Reference number: S41941
 A:Accession: S41941
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-382 <GON>
 A:Cross-References: EMBL:X77455; NID:g453214; PIDN:CA54602.1; PID:g453215
 C:Superfamily: Escherichia coli beta-lactamase
 S41941 Length: 382 March 17, 2003 12:10 Type: P Check: 7779 ..
 Found using 'KTXS' (swope073.key)

196 SOTLLPKLGHHTYIQVPESAIANTAYGSKEDKPVRTPGVLAEAAYGKTKGSADLLKF
 246

256 TEANNMGYGDAAALKTRIALTHRTGYFVSGDMTQGLGMEYAYPLTEQALLAGNSPAVSFOA

316 NPVTRPAVFKAMGEORLYNKGTSGTGFGAYVAFVARGIAIVMLANRNPTEARVKAHAH
 335

376 ILSQLAE

2 matches found in sequence:
 S44080 : TOIG of: S44080 check: 7397 from: 1 to: 294
 (from "lactxs_pir.pep")
 TOIG of: S44080 check: 7397 from: 1 to: 294

PI:S44080 - beta-lactamase (EC 3.5.2.6) BPL-1 - Serratia marcescens
 C:Species: Serratia marcescens
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1995
 C:Accession: S44080; S49165
 R:Naas, T.; Vandel, L.; Livermore, D.; Nordmann, P.
 Submitted to the EMBL Data Library, December 1993
 A:Description: Cloning and sequence analysis of the Carbapenem-hydrolysing
 class A'-lactamase from Serratia marcescens S6 clinical isolate.
 A:Reference number: S44080
 A:Accession: S44080
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-294 <NAA>
 A:Cross-References: EMBL:Z28968; NID:g472863; PIDN:CA82281.1; PID:g472864
 R:Naas, T.; Vandel, L.; Sougkoff, W.; Livermore, D.M.; Nordmann, P.
 Submitted to the EMBL Data Library, February 1994
 A:Description: Cloning and sequence analysis of the carbapenem-hydrolysing
 class A beta-lactamase, Bp1A, from Serratia marcescens S6.
 A:Reference number: S49164
 A:Accession: S49165
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-31 <NA2>
 A:Cross-References: EMBL:Z30237
 C:Superfamily: beta-lactamase I
 C:Keywords: hydrolase
 S44080 Length: 294 March 17, 2003 12:10 Type: P Check: 7397 ..
 Found using 'KTXS' (swope073.key)

1 MSKNVNFKTASFLFVCLALSAFNHANKSDAAKQIKLEEDFDGRIGVAFIDTSGNT
 8 11

61 F

...

188 KAVANSINKLALGNVLANKVKAIYQNWILKNTGDRIRASVPADWVGDGTGSGALGT
 238

248 ANDYAVIWPKNRABLIVSIYTRKSKDDKHSDKTIAESRIATQ

1 match found in sequence:
 S44094 : TOIG of: S44094 check: 450 from: 1 to: 381
 (from "lactxs_pir.pep")
 TOIG of: S44094 check: 450 from: 1 to: 381

PI:S44094 - beta-lactamase (EC 3.5.2.6) - Citrobacter freundii
 C:Species: Citrobacter freundii
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1995
 C:Accession: S44094
 R:Benet, P.M.; Damdinuren, E.; Jones, M.F.
 Submitted to the EMBL Data Library, December 1993
 A:Reference number: S44094
 A:Accession: S44094
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-381 <BPN>

A:Cross-References: EMBL:X76636; NID:g472907; PIDN:CA54084.1; PID:g472908
 C:Superfamily: Escherichia coli beta-lactamase
 C:Keywords: hydrolase
 F:84/Active site: Ser #status predicted

S44094 Length: 381 March 17, 2003 12:10 Type: P Check: 450 ..
 Found using 'KTXS' (swope073.key)

285 MYOGLGWEMLNWPVKADIVINGSDSKITALALPAVEVNPAPVYKASWVKGTSGFGS
 335

345 YVAFIPEKNIGIYMLANKSYNPARVDAMRIIEKIQ

1 match found in sequence:
 S45109 : TOIG of: S45109 check: 488 from: 1 to: 381
 (from "lactxs_pir.pep")
 TOIG of: S45109 check: 488 from: 1 to: 381

PI:S45109 - beta-lactamase (EC 3.5.2.6) precursor - Klebsiella pneumoniae
 C:Species: Klebsiella pneumoniae
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1995
 C:Accession: S45109
 R:Tzouvelektis, L.S.; Tzelepi, E.; Mentis, A.F.
 Submitted to the EMBL Data Library, March 1994
 A:Description: Nucleotide sequence of a plasmidic cephalosporinase gene
 (bla-LAT-1) found in Klebsiella pneumoniae.
 A:Reference number: S45109
 A:Accession: S45109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-381 <TZO>
 A:Cross-References: EMBL:X78117; NID:g496632; PIDN:CA55007.1; PID:g496633
 C:Superfamily: Escherichia coli beta-lactamase
 C:Keywords: hydrolase
 F:84/Active site: Ser #status predicted

S45109 Length: 381 March 17, 2003 12:10 Type: P Check: 488 ..
 Found using 'KTXS' (swope073.key)

285 MYOGLGWEMLNWPVKADSIINGSDSKVALAALPAVEVNPAPVYKASWVKGTSGFGS
 335

345 YVAFVPEKNIGIYMLANKSYNPARVDAMRIIEKIQ

1 match found in sequence:
 s49543 : TOIG of: s49543 check: 7122 from: 1 to: 271
 (from "lactxs_pir.pep")
 TOIG of: s49543 check: 7122 from: 1 to: 271

PI:s49543 - beta-lactamase - Proteus vulgaris
 C:Species: Proteus vulgaris
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
 C:Accession: S47620
 R:Rezzazi, J.; Keynaud, A.; Baron, P.; Barthelemy, M.; Labia, R.
 Biochim. Biophys. Acta 1207, 31-39, 1994
 A:Title: Chromosomally encoded cephalosporin-hydrolyzing beta-lactamase of
 Proteus vulgaris RO104 belongs to Ambler's class A.
 A:Reference number: S47620; MUID:94318667; PMID:8043607
 A:Accession: S47620
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-271 <PBD>
 C:Superfamily: beta-lactamase I

S47620 Length: 271 March 17, 2003 12:10 Type: P Check: 7122
 Found using 'KTXS' (swope073.key)

160 IMAKSLQALTLGDALGSGRQQLVTLKNGTGDHSIKAGLPKHWIVGDKTSGDYGTT
 210

220 NDIAVIMPKNHAPLILVYFTQOEODAKYRKDIYKATEIYVKE

1 match found in sequence:
 s49543 : TOIG of: s49543 check: 5458 from: 1 to: 294
 (from "lactxs_pir.pep")
 TOIG of: s49543 check: 5458 from: 1 to: 294

PI:s49543 - beta-lactamase (EC 3.5.2.6) class A precursor - Mycobacterium
 fortuitum (strain FCI)
 C:Species: Mycobacterium fortuitum
 A:Variety: strain FCI
 C>Date: 15-Feb-1996 #sequence_revision 27-Feb-1997 #text_change 22-Jun-1999
 C:Accession: S49543
 R:Timm, J.; Perilli, M.G.; Duez, C.; Trias, J.; Orfichi, G.; Fattorini, L.;
 Amicosante, G.; Oratore, A.; Joris, B.; Frere, J.M.; Pugsley, A.P.; Gicquel, B.
 Mol. Microbiol. 12, 491-504, 1994
 A:Title: Transcription and expression analysis, using lacZ and phoA gene
 fusions, of Mycobacterium fortuitum beta-lactamase genes cloned from a natural
 isolate and a high-level beta-lactamase producer.
 A:Reference number: S49543; MUID:94344037; PMID:8065266
 A:Accession: S49543
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-294 <TIM>
 A:Cross-references: EMBL:L25634; NID:9497607; PIDN:AAA19882.1; PID:9497608
 A:Experimental source: strain FCI
 A>Note: the sequence of residues 289-294 and the corresponding nucleotide
 sequence are not shown in this paper
 C:Genetics:
 A:Gene: blaF
 C:Superfamily: beta-lactamase I
 C:Keywords: antibiotic resistance; extracellular protein; hydrolase
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:33-294/Product: beta-lactamase class A #status predicted <MAT>

S49543 Length: 294 March 17, 2003 12:10 Type: P Check: 5458
 Found using 'KTXS' (swope073.key)

187 TAAALAVGYRAILAGDALSPQRLLEDWMRANQSSMRAGLPBGWTTADKTGSDYGST
 237

247 NDAIGAFPGDQRLILVMMTRSOAHPKAEHLRPLIGELTALVL

1 match found in sequence:
 S51044 : TOIG of: S51044 check: 3746 from: 1 to: 300
 (from "lactxs_pir.pep")
 TOIG of: S51044 check: 3746 from: 1 to: 300

PI:S51044 - beta-lactamase - Proteus vulgaris
 C:Species: Proteus vulgaris
 C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999
 C:Accession: S51044
 R:Datz, M.; Joris, B.; Azab, E.A.M.; Galleni, M.; van Beeumen, J.; Frere, J.M.;
 Martin, H.H.
 Eur. J. Biochem. 226, 149-157, 1994
 A:Title: A common system controls the induction of very different genes. The
 class A beta-lactamase of Proteus vulgaris and the enterobacterial class-C
 beta-lactamase.
 A:Reference number: S51044; MUID:95045583; PMID:7957242
 A:Accession: S51044
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-300 <DAT>
 A:Cross-references: EMBL:X80128; NID:9511055; PIDN:CAA56427.1; PID:9511056
 C:Superfamily: beta-lactamase I

S51044 Length: 300 March 17, 2003 12:10 Type: P Check: 3746
 Found using 'KTXS' (swope073.key)

189 IMAKSLQALTLGDALGSGRQQLVTLKNGTGDHSIKAGLPKHWIVGDKTSGDYGTT
 239

249 NDIAVIMPKNHAPLILVYFTQOEODAKYRKDIYKATEIYVKE

1 match found in sequence:
 S54103 : TOIG of: S54103 check: 3376 from: 1 to: 385
 (from "lactxs_pir.pep")
 TOIG of: S54103 check: 3376 from: 1 to: 385

PI:S54103 - beta-lactamase (EC 3.5.2.6) - Lysobacter lactamgenus (strain YK90)
 C:Species: Lysobacter lactamgenus
 A:Variety: strain YK90
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
 C:Accession: S54103
 R:Kimura, H.; Iwawa, M.; Miyashita, H.; Shimizu, Y.; Sunino, Y.; Suzuki, M.
 submitted to the EMBL Data Library, October 1990
 A:Description: Gene cluster involved in the cephalosporin biosynthesis from
 Lysobacter lactamgenus YK90.
 A:Reference number: S54099
 A:Accession: S54103
 A:Molecule type: DNA
 A:Residues: 1-385 <KIM>
 A:Cross-references: EMBL:X56660; NID:9769806; PIDN:CAA39987.1; PID:9769811
 A:Experimental source: strain YK90
 C:Superfamily: Escherichia coli beta-lactamase
 C:Keywords: antibiotic biosynthesis; hydrolase

S54103 Length: 385 March 17, 2003 12:10 Type: P Check: 3376
 Found using 'KTXS' (swope073.key)

285 MTQGLWEQLPYPASETSLQANSSQKVFESNAVALTPPPPPQANVLINKTGRFGA
335

345 YVAFNPARKIGIVLMNRVPMGRKILAHITLDTAGGMAK

1 match found in sequence:
s56942 ; TOIG of: s56942 check: 2987 from: 1 to: 310
(from "ktxs_pir.pir")
TOIG of: s56942 check: 2987 from: 1 to: 310

PI:S56942 - heat shock protein HSP150 (version 1) - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein J0558; protein YJL159w

C:Species: Saccharomyces cerevisiae

C>Date: 05-May-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002

C:Accession: S56942; S60370

R:Obermaler, B.; Piravandi, E.; Rinke, M.; Domdey, H.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56937

A:Accession: S56942

A:Molecule type: DNA

A:Residues: 1-310 <OBE>

A:Cross-references: EMBL:Z49434; NID:q1015582; PIDN:CA89454.1; PID:q1015583;

MIPS:YJL159w

R:Jaamsa, E.; Holkeri, H.; Vihnen, H.; Wikstrom, M.; Simonen, M.; Walse, B.;

Kalkkinen, N.; Paakkola, J.; Makarow, M.

Yeast 11, 1381-1391, 1995

A:Title: Structural features of a polypeptide carrier promoting secretion of a

beta-lactamase fusion protein in yeast.

A:Reference number: S60370; MID:96158058; PMID:8585321

A:Accession: S60370

A:Molecule type: protein

A:Residues: 19-31; 73-85 <JAE>

C:Genetics:

A:Gene: SGD:HSP150; HSP150; PIR2

A:Cross-references: MIPS:YJL159w; SGD:S0003695

A:Map position: 10L

S56942 Length: 310 March 17, 2003 12:10 Type: P Check: 2987 ..

Found using 'KTXS' (swop073.key)

80 GQVQAAATTASVSTKSTAAVSGIDGQIQATTTTAAVSRDQIQATTTKTTSAKTAA
130

140 AVSQISDQIQATTTTLAPKSTAAVSGIDGQVQATTTTAA

-- Search Statistics --

Times: CPU Total Elapsed
00:00:00.02 00:00:02.00

Number of sequences searched: 34
Number of sequence hits: 34
Number of separate matches: 38
Number of sequence hits saved: 0

2
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v
C

Quest - Quick User-directed Expression Search Tool
Release 5.4

ID AMPC_ENTCL STANDARD: PRT; 381 AA.
AC P05364;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase).
GN AmpC.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_Taxid=550;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P99, Q908R, and MHNI;
RX MEDLINE=88268750; PubMed=3260487;
RA Galleni M., Lindberg F., Normark S., Cole S., Honore N., Joris B.,
RA Frere J.-M.;
RT "Sequence and comparative analysis of three Enterobacter cloacae ampC
RT beta-lactamase genes and their products.";
RT Biochem. J. 250:753-760(1988).
RN [2]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RP STRAIN=P99.
RC MEDLINE=94068583; PubMed=8248237;
RX Lobkovsky E., Moews P.C., Liu H., Zhao H., Frere J.-M., Knox J.R.;
RT "Evolution of an enzyme activity: crystallographic structure at 2-A
RT resolution of cephalosporinase from the ampC gene of Enterobacter
RT cloacae P99 and comparison with a class A penicillinase.";
RT Proc. Natl. Acad. Sci. U.S.A. 90:11257-11261(1993).
RN [3]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RP STRAIN=P99;
RX MEDLINE=94263990; PubMed=8204611;
RA Lobkovsky E., Billings E.M., Moews P.C., Rahl J., Pratt R.F.,
RA Knox J.R.;
RT "Crystallographic structure of a phosphonate derivative of the
RT Enterobacter cloacae P99 cephalosporinase: mechanistic interpretation
RT of a beta-lactamase transition-state analog.";
RL Biochemistry 33:6762-6772(1994).
CC -1- FUNCTION: THIS PROTEIN IS A SERINE BETA-LACTAMASE WITH A SUBSTRATE
CC SPECIFICITY FOR CEPHALOSPORINS.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -1- SIMILARITY: THE SEQUENCE SHOWN IS THAT OF STRAIN P99.
CC -1- SIMILARITY: BELONGS TO THE CLASS-C BETA-LACTAMASE FAMILY.
CC -----
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CC -----
DR EMBL: X07274; CAA30257.1; -
DR EMBL: X08082; CAA30879.1; -
DR EMBL: X08081; CAA30878.1; -
DR PIR: S00404; PNRKP.
DR PIR: S00405; PNRBO.
DR PIR: S00406; PNRBM.
DR PDB: 1BL5; 08-MAY-95.
DR PDB: 2BLT; 26-JAN-95.
DR MEROPS: S12.UMW; -
DR InterPro: IPR001466; Beta_Lactamase.
DR InterPro: IPR001586; Beta_Lactamase.C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW Hydrolyase; Antibiotic resistance; Periplasmic; Signal; 3D-structure.
FT SIGNAL 1 20
FT CHAIN 21 381 BETA-LACTAMASE.
FT ACT_SITE 84 84
FT BINDING 335 337 SUBSTRATE.

FT VARIANT 3 3 R -> I (IN STRAIN MHNI).
FT VARIANT 14 14 I -> L (IN STRAIN MHNI).
FT VARIANT 21 21 T -> A (IN STRAIN MHNI).
FT VARIANT 36 36 I -> V (IN STRAIN MHNI AND Q980R).
FT VARIANT 58 58 P -> S (IN STRAIN MHNI).
FT VARIANT 108 108 A -> P (IN STRAINS MHNI AND Q980R).
FT VARIANT 152 152 L -> V (IN STRAIN Q980R).
FT VARIANT 262 262 N -> K (IN STRAIN MHNI).
FT VARIANT 319 319 A -> V (IN STRAIN Q980R).
FT VARIANT 362 362 T -> K (IN STRAIN MHNI).
SQ SEQUENCE 381 AA; 41301 MW; 90F56ABAF07AA304 CRC64;
AMPC_ENTCL Length: 381 March 17, 2003 12:16 Type: P Check: 735 ..
Found using 'KTXS' (swop073.key)
285 MYOGLGEMLMNPVEANTVVEGSDSKVALAPLPVAEVPNPAPPVKASWVHKGTGSGFGS
335
345 YVAFPEKQIGIVMANTSTPNPAREVAHIIIEALQ

1 match found in sequence:
ampClys1 : Beta-lactamase precursor (EC 3.5.2.6) (cephalosporinase).
(from "ktxs_sp.pep")
TOIG of: ampC_Lys1a check: 3376 from: 1 to: 385
ID AMPC_LYS1A STANDARD: PRT; 385 AA.
AC Q48743;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase).
OS Lysobacter lactangenus.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Lysobacter.
OX NCBI_Taxid=39596;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=YK90;
RX MEDLINE=96287475; PubMed=8703429;
RA Kimura H., Izawa M., Sumino Y.;
RT "Molecular analysis of the gene cluster involved in cephalosporin
RT biosynthesis from Lysobacter lactangenus YK90.";
RL Appl. Microbiol. Biotechnol. 44:589-596(1996).
CC -1- FUNCTION: THIS PROTEIN IS A SERINE BETA-LACTAMASE WITH A
CC SUBSTRATE SPECIFICITY FOR CEPHALOSPORINS.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE CLASS-C BETA-LACTAMASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56660; CAA39987.1; -
DR PIR: S54103; S54103.
DR HSSP: P05364; 2BLT.
DR MEROPS: S12.UMW; -
DR InterPro: IPR001466; Beta_Lactamase.
DR InterPro: IPR001586; Beta_Lactamase.C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW Hydrolyase; Antibiotic resistance; Periplasmic; Signal.
FT SIGNAL 1 20
FT CHAIN 21 385 BY SIMILARITY.
FT BINDING 335 337 BETA-LACTAMASE.

FT ACT SITE 84 84 BY SIMILARITY.
 FT BINDING 335 337 SUBSTRATE (BY SIMILARITY).
 SQ SEQUENCE 385 AA: 41878 MW: 33DA95118EC28207 CRC64;

AMPC_LXSLA Length: 385 March 17, 2003 12:16 Type: P Check: 3376
 Found using 'KTXS' (swope073.key)

285 MGQGLVWELPPASETSIQANSSQKVFESNAVALPPPPQANLVNTGSGRGGA
 335

345 YVAFNPARKIGIVLLNRSVPMQGRKILAHITLDTAGMAX

1 match found in sequence:
 ampcprost : Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase).
 (from "lactxs_sp.pep")
 TOIG of: ampc_prost check: 6628 from: 1 to: 384

ID AMPC_PROST STANDARD: PRT: 384 AA.
 AC 069773;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase).
 GN AMPC.

OS Providencia stuartii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Providencia.
 OX NCBI_TaxID=588;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VDG 96;
 RA Koeck J.L., Basmaciogullari S., Parzy D., Barnaud G., Teyssou R.,
 RA Buisson Y., Philippot A., Arlet G.J.;

RT "Cloning and sequencing of ampc and ampr genes from Providencia
 stuartii".

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN IS A SERINE BETA-LACTAMASE WITH A
 SUBSTRATE SPECIFICITY FOR CEPHALOSPORINS.

CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 amino acid.

CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CLASS-C BETA-LACTAMASE FAMILY.

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CC EMBL: Y17315; CAA76739.1; -
 CC HSSP: P05364; 2BLT.
 DR InterPro: IPR001466; Beta_Lactamase.
 DR InterPro: IPR001586; Beta_Lactamase_C.

DR Pfam: PF00144; Beta_Lactamase_1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; FALSE_NEG.

KW Hydrophobic; Antibiotic resistance; Periplasmic; Signal.
 FT SIGNAL 1 29 POTENTIAL.

FT CHAIN 30 384 BETA-LACTAMASE.
 FT ACT SITE 87 87 BY SIMILARITY.

FT BINDING 337 339 SUBSTRATE (BY SIMILARITY).
 SQ SEQUENCE 384 AA: 43366 MW: 8CCAC7F9B1377B9 CRC64;

AMPC_PROST Length: 384 March 17, 2003 12:16 Type: P Check: 6628
 Found using 'KTXS' (swope073.key)

287 FVQDMWESYPMVPSLSQLQGNRDMALKPKQVELIKPAMAPPRVARYVKKSGSGNFAT
 337

347 YAFIPEKIALVMSKNKWIPIQRTATYQLEKIER

1 match found in sequence:
 ampcpsae : Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase).
 (from "lactxs_sp.pep")
 TOIG of: ampc_pseae check: 9146 from: 1 to: 397

ID AMPC_PSEAE STANDARD: PRT: 397 AA.
 AC P24735;

DT 01-MAR-1992 (Rel. 21, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase).
 GN AMPC OR PA4110.
 OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.

OX NCBI_TaxID=287;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01:
 RX MEDLINE=20437337; PubMed=10984043;
 RA Slover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen."
 RL Biochem. J. 272:627-631(1990).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01:
 RX MEDLINE=94282208; PubMed=8012497;
 RA Michael-Hamzehpour M., Sanchez J.-C., Epp S.F., Paquet N., Hughes G.J.,
 RA Hochstrasser D.F., Pecheux J.-C.;
 RT "Two-dimensional polyacrylamide gel electrophoresis isolation and
 RT microsequencing of Pseudomonas aeruginosa proteins."
 RL Enzyme Protein 47:1-8(1993).

RN [4]
 RP SEQUENCE OF 1-3 FROM N.A.
 RC STRAIN=ATCC 15692 / PA01:
 RX MEDLINE=94010221; PubMed=8405939;
 RA Lodge J.M., Busby S.J.W., Piddock L.J.V.;
 RT "Investigation of the Pseudomonas aeruginosa ampr gene and its role
 RT at the chromosomal ampc beta-lactamase promoter."
 RL FEMS Microbiol. Lett. 111:315-320(1993).

CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 amino acid
 CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CLASS-C BETA-LACTAMASE FAMILY.

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CC -----
DR EMBL: X54719; CAA38522.1; -.
DR EMBL: AE004827; AAC07497.1; -.
DR EMBL: X67095; CAA47469.1; -.
DR PIR: S13408; S13408.
DR HSSP: P05364; 2BLT.
DR MEROPS: S12.UNW; -.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase.C.
DR Pfam: PF00144; beta_lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE; 1.
KW Hydrolyase; Antibiotic resistance; Periplasmic; Signal;
KW Complete proteome.
FT SIGNAL 1 26
FT CHAIN 27 397 BETA-LACTAMASE.
FT ACT SITE 90 90 BY SIMILARITY.
FT BINDING 342 344 SUBSTRATE (BY SIMILARITY).
FT CONFLICT 397 397 R -> A (IN REF. 1).
SQ SEQUENCE 397 AA; 43401 MW; C6341A53594BC261 CRC64;

AMPC_PSEAE Length: 397 March 17, 2003 12:16 Type: P Check: 9146 ..
Found using 'KTXS' (swope073.key)

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292 MTGIGWEAYWPISLKRLQAGNSTPMALOPHRIARLPAPQALGEGORLLNKGSTNGFGA
|---|
352 YVAFVPGRDGLVILANRNYNAERVKIAYAILSGLEQGVPL
342

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1 match found in sequence:
ampcserma; Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase).
(from "lactxs.sp.pep")
TOIG of: ampc_serma check: 107 from: 1 to: 376

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```

ID AMPC_SERMA STANDARD; PRT; 376 AA.
AC P18539;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase).
GN AMP.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SR50;
RX MEDLINE=91032898; PubMed=2227264;
RT Nomura K., Yoshida T.;
RT "Nucleotide sequence of the Serratia marcescens SR50 chromosomal ampc
beta-lactamase gene.";
RL FEMS Microbiol. Lett. 58:295-299(1990).
CC -1- FUNCTION: THIS PROTEIN IS A SERINE BETA-LACTAMASE WITH A SUBSTRATE
CC SPECIFICITY FOR CEPHALOSPORINS.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE CLASS-C BETA-LACTAMASE FAMILY.
CC
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DR EMBL: X52964; CAA37137.1; -.
DR PIR: S11710; OKSE.
DR PIR: A48176; A48176.
DR HSSP: P05364; 2BLT.
DR MEROPS: S12.UNW; -.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase.C.
DR Pfam: PF00144; beta_lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE; 1.
KW Hydrolyase; Antibiotic resistance; Periplasmic; Signal.
KW Complete proteome.
FT SIGNAL 1 21
FT CHAIN 22 376 BETA-LACTAMASE.
FT ACT SITE 79 79 BY SIMILARITY.
FT BINDING 328 330 SUBSTRATE (BY SIMILARITY).
SQ SEQUENCE 376 AA; 41096 MW; 890CEE7C27925150 CRC64;

AMPC_SERMA Length: 376 March 17, 2003 12:16 Type: P Check: 107 ..
Found using 'KTXS' (swope073.key)

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278 FTQDLMWENYPPVVKLSRLIEGNNAGIMNGTPATATPPQELBAGWYKTKGTGFST
|---|
338 YVAFIPAKNINAVEMLANKMFPPNDRVEAYVHIQALEKR
328

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```

1 match found in sequence:
blalacery; Beta-lactamase AER-1 precursor (EC 3.5.2.6) (Penicillinase).
(from "lactxs.sp.pep")
TOIG of: blalacery check: 7808 from: 1 to: 304

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```

ID BLAL_AERHY STANDARD; PRT; 304 AA.
AC Q44056;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-lactamase AER-1 precursor (EC 3.5.2.6) (Penicillinase).
GN AER1.
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
OC Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VL7711; TRANSPOSON=Omega7711;
RX MEDLINE=98353319; PubMed=9687391;
RA Sanschagrin F., Bejaoui N., Levesque R.C.;
RT "Structure of CARB-4 and AER-1 carbenicillin-hydrolyzing beta-
lactamases.";
RT Antimicrob. Agents Chemother. 42:1966-1972(1998).
RL Antimicrob. Agents Chemother. 42:1966-1972(1998).
CC -1- FUNCTION: HYDROLYZES CARBENICILLIN, METHICILLIN AND OXACILLIN ARE
CC WEAKLY HYDROLYZED.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC
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CC
CC EMBL: U14748; AAC09015.1; -.
CC HSSP: P14557; 1SHV.
CC InterPro: IPR001466; Beta_lactamase.
CC InterPro: IPR000871; Beta_lactamase_A.
CC Pfam: PF00144; beta_lactamase; 1.
CC PRINTS: PR00118; BLACTAMASEA.
CC PROSITE: PS00146; BETA_LACTAMASE_A; 1.

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KW Hydrolase; Antibiotic resistance; Signal; Transposable element.
FT SIGNAL 1 37
FT CHAIN 38 304
FT ACT_SITE 83 83
FT DISULFID 90 137
FT BINDING 248 250
SQ SEQUENCE 304 AA; 32428 MW; 66AD56ED45D02A41 CRC64;

BLAL AERRY Length: 304 March 17, 2003 12:16 Type: P Check: 7808 ..
Found using 'KTXS' (swope073.key)

...
36 FALDTKLIQAVQSEESALHARVGMVDPDNTGTTWNRGDERPFLNTHKTFSCAALLA 1--1
66 89
66 KVDGKSLSGQSVSISKEMLVYSPTEKSLSPETVTFGKICQA

1 match found in sequence:
blaxxama ; Beta-lactamase L2 precursor (EC 3.5.2.6) (Penicillinase).
(from "lactxs_sp.pep")
TOIG of: blax2_xanna check: 5580 from: 1 to: 303

ID BLA2_XANNA STANDARD; PRT; 303 AA.
AC P96465;
AD 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-lactamase L2 precursor (EC 3.5.2.6) (Penicillinase).
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
malophilila).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IID 1275;
RX MEDLINE=97354372; PubMed=9210666;
RA Walsh T.R., Macgowan A.P., Bennett P.M.;
RT "Sequence analysis and enzyme kinetics of the L2 serine beta-lactamase
from Stenotrophomonas maltophilia.";
RL Antimicrob. Agents Chemother. 41:1460-1464(1997).
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O -> a substituted beta-
amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
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CC -----
CC EMBL; Y08562; CAA69869.1; -.
DR HSSP; 047066; 1BZA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase_1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolase; Antibiotic resistance; Signal.
FT SIGNAL 1 20
FT CHAIN 21 303
FT ACT_SITE 83 83
FT BINDING 247 249
SQ SEQUENCE 303 AA; 32207 MW; C278DAFAC824FDD3C CRC64;

BLA2_XANNA Length: 303 March 17, 2003 12:16 Type: P Check: 5580 ..

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Found using 'KTXS' (swope073.key)

...
197 AAMATLQRVGLGEVLQIASRQQLADWLIDNETGDACLKGLKLMVRDKTSGNGEDAR 1--1
247
257 NDIAVMPVAGGAPWLVLTAVLQAGAISTEORATVLAOVGRIADR

1 match found in sequence:
blabprovu ; Beta-lactamase precursor (EC 3.5.2.6) (Cefuroximease).
(from "lactxs_sp.pep")
TOIG of: blab_provuv check: 3746 from: 1 to: 300

ID BLAB_PROVU STANDARD; PRT; 300 AA.
AC P52664;
AD 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-lactamase precursor (EC 3.5.2.6) (Cefuroximease).
GN BLAB OR CUMA.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B317;
RX MEDLINE=95045583; PubMed=7957242;
RA Datz M., Joris B., Azab E.A., Galleni M., van Beeumen J., Frere J.-M.,
RA Martin H.H.;
RT "A common system controls the induction of very different genes. The
RT class-A beta-lactamase of Proteus vulgaris and the enterobacterial
RT class-C beta-lactamase.";
RL Eur. J. Biochem. 226:149-157(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=5E78-1;
RA Okuguchi M., Komai T., Makajima N., Eguchi H., Kuboki A., Ito T.,
RA Meguro M., Nakata T., Sugimoto K.;
RT Submitted (JUG-1994) to the EMBL/GenBank/ODDB databases.
CC -1- FUNCTION: HYDROLYZES BROAD-SPECTRUM BETA-LACTAM ANTIBIOTICS.
CC ACTIVE AGAINST CEFHALOSPORINS SUCH AS CEFUROXIME AND CEFOTAXIME.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O -> a substituted beta-
amino acid.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC -----
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CC -----
CC EMBL; X80128; CAA56427.1; -.
DR EMBL; D37831; BAA07084.1; -.
DR HSSP; 047066; 1BZA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolase; Antibiotic resistance; Signal.
FT SIGNAL 1 29
FT CHAIN 30 300
FT ACT_SITE 75 75
FT BINDING 239 241
SQ SEQUENCE 300 AA; 32411 MW; 66AD56ED45D02A41 CRC64;

BLA2_XANNA Length: 303 March 17, 2003 12:16 Type: P Check: 5580 ..

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FT  VARIANT  13      13      T -> A (IN STRAIN 5E78-1).
FT  VARIANT  23      23      V -> A (IN STRAIN 5E78-1).
FT  VARIANT  30      31      NT -> DN (IN STRAIN 5E78-1).
FT  VARIANT  40      40      S -> N (IN STRAIN 5E78-1).
FT  VARIANT  58      58      E -> K (IN STRAIN 5E78-1).
FT  VARIANT  88      88      E -> A (IN STRAIN 5E78-1).
FT  VARIANT  119     119     S -> T (IN STRAIN 5E78-1).
FT  VARIANT  123     123     V -> T (IN STRAIN 5E78-1).
FT  VARIANT  126     126     Q -> E (IN STRAIN 5E78-1).
FT  VARIANT  224     224     H -> N (IN STRAIN 5E78-1).
FT  VARIANT  235     235     I -> V (IN STRAIN 5E78-1).
FT  VARIANT  257     257     K -> E (IN STRAIN 5E78-1).
FT  VARIANT  283     283     V -> A (IN STRAIN 5E78-1).
FT  VARIANT  286     286     T -> A (IN STRAIN 5E78-1).
SQ  SEQUENCE  300 AA; 32991 MW; 2719AF2464F1CD77 CRC64;

BLAB_PROVU Length: 300 March 17, 2003 12:16 Type: P Check: 3746
Found using 'KTxs' (swope073.key)

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189  IMAKSLQALVTLGDALGOSORQOLVYWLKNGTGDHSIKALPKLHVIQDKTSGDYGT
      239
      1--1

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249  NDIAVIMPKNHAPLIVVFTQEQDQAKYRKDIIVKATEIVTKE

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```

1 match found in sequence:
blachacu ; Beta-lactamase precursor (EC 3.5.2.6).
(from "lactxs_sp.pep")

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TOIG of: blac_bacun check: 1067 from: 1 to: 296

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ID  BLAC_BACUN  STANDARD;  PRT;  296 AA.
AC  P30898;
DT  01-JUL-1993 (Rel. 26, Created)
DT  01-JUL-1993 (Rel. 26, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Beta-lactamase precursor (EC 3.5.2.6).
GN  CBLA.
OS  Bacteroides uniformis.
OC  Bacteria: Bacteroidetes; Bacteroides; Bacteroidales; Bacteroidaceae;
CC  Bacteroides
CN  NCBI_TaxID=820;
RX  MEDLINE=95077321; PubMed=7985999;
RA  Smith C.J., Bennett T.K., Parker A.C.;
RT  "Molecular and genetic analysis of the Bacteroides uniformis
RT  cephalosporinase gene, cblA, encoding the species-specific beta-
RT  lactamase."
RL  Antimicrob. Agents Chemother. 38:1711-1715(1994).
CC  -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O - a substituted beta-
CC  amino acid.
CC  -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; L08472; AAA66962.1; -
DR  InterPro: IPR001466; Beta_lactamase.
DR  InterPro: IPR000871; Beta_lactamase_A.
DR  Pfam; PF00144; beta_lactamase; 1.
DR  PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW  Hydrolyase; Antibiolic resistance; Signal.

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FT  SIGNAL  1      21      POTENTIAL.
FT  CHAIN  22      296      BETA-LACTAMASE.
FT  ACT SITE  66      66      BY SIMILARITY.
FT  BINDING  235     237     SUBSTRATE (BY SIMILARITY).
SQ  SEQUENCE  296 AA; 33450 MW; 87ACA38331207004 CRC64;

BLAB_PROVU Length: 296 March 17, 2003 12:16 Type: P Check: 1067
Found using 'KTxs' (swope073.key)

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185  AMVRLRTADEKEKLPNSKELDFIMQIMIDFETGANKLKMLPAKTYVGHTGSSDRNAD
      235
      1--1

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245  GMKATNDAGVILIPDGKRYIAAFVMSYEDDNANIARIIS

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2 matches found in sequence:
blachacu ; Beta-lactamase precursor (EC 3.5.2.6).
(from "lactxs_sp.pep")
TOIG of: blac_bacvu check: 4541 from: 1 to: 321

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ID  BLAC_BACVU  STANDARD;  PRT;  321 AA.
AC  P30899;
DT  01-JUL-1993 (Rel. 26, Created)
DT  01-JUL-1993 (Rel. 26, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  Beta-lactamase precursor (EC 3.5.2.6).
GN  CFXA.
OS  Bacteroides vulgatus.
OC  Bacteria: Bacteroidetes; Bacteroides; Bacteroidales; Bacteroidaceae;
CC  Bacteroides
CN  NCBI_TaxID=821;
RX  MEDLINE=93297917; PubMed=8517690;
RA  Parker A.C., Smith C.J.;
RT  "Genetic and biochemical analysis of a novel Ambler class A beta-
RT  lactamase responsible for cefoxitin resistance in Bacteroides
RT  species."
RL  Antimicrob. Agents Chemother. 37:1028-1036(1993).
CC  -1- FUNCTION: CAN HYDROLYZE CEPHALOSPORINS, PENICILLINS AND ALSO
CC  CEROXITIN. BUT AT A SLOW RATE.
CC  -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O - a substituted beta-
CC  amino acid.
CC  -1- ENZYME REGULATION: INHIBITED BY CLAVULANIC ACID.
CC  -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U38243; AAB17891.1; -
DR  PIR; S27528; S27528.
DR  InterPro: IPR001466; Beta_lactamase.
DR  InterPro: IPR000871; Beta_lactamase_A.
DR  Pfam; PF00144; beta_lactamase; 1.
DR  PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW  Hydrolyase; Antibiolic resistance; Signal.
FT  SIGNAL  1      30      POTENTIAL.
FT  CHAIN  31      321      BETA-LACTAMASE.
FT  ACT SITE  83      83      BY SIMILARITY.
FT  BINDING  233     235     SUBSTRATE (BY SIMILARITY).
SQ  SEQUENCE  321 AA; 35375 MW; 6ADD45ED16F0BDFA CRC64;

```


BLAC_BACVU Length: 321 March 17, 2003 12:16 Type: P Check: 4541 ..
Found using 'KTxs' (swope073.key)

68 RDTVKVNSKSVPMMSVFKVQALALCNDNFNGKISLDTLVNINRDKLPKTPWSPMLKDY
118

128 SGPVISITVVDLRLTYLTOSDNNASLMFKDMVYNAQTSFIAT

204 AAMLNRLFTFEGILIDDEKOSFIKNTLKECKTGVDRIAPLDEKGVYIAHKGSGGVNEN
254

264 GVLAHNDVAYICLPNNISYTLAVFVKFKNGKNSQASQYVAHIS

1 match found in sequence:
blacnolia ; Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).
(from "lactxs_sp.pep")
TOIG of: blac_nolia check: 8442 from: 1 to: 302

ID BLAC_NOLIA STANDARD; PRT; 302 AA.
AC 006316;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).
GN BLA.

OS Nocardia lactamdurans.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Pseudonocardiales; Pseudonocardaceae;
OC Amycolatopsids.
OX NCBI_TaxID=1913;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=LC411;
RX MEDLINE=93178438; PubMed=8440253;

RA Coque J.J.R., Liras P., Martin J.F.;

RT "Genes for a beta-lactamase, a penicillin-binding protein and a
transmembrane protein are clustered with the cephamycin biosynthetic
genes in Nocardia lactamdurans.";

RL EMBO J. 12:631-639(1993).

CC -1- FUNCTION: ACTIVE ON PENICILLINS BUT NOT ON CEPHALOSPORINS.

CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
amino acid.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.

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or send an email to license@isb-sib.ch).

CC EMBL: Z13971; CAA78373.1; ..

DR HSSP: P00808; 4BLM.

DR InterPro: IPR001466; Beta_lactamase.

DR InterPro: IPR000871; Beta_lactamase_A.

DR Pfam: PF00144; beta-lactamase; 1.

DR PRINTS: PR00118; BLACTAMASEA.

DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.

KW Hydrolase; Antibiotic resistance; Signal.

FT CHAIN 1 29
FT SIGNAL 1 29
FT ACT_SITE 85 85 BETA-LACTAMASE.
BY SIMILARITY.

FT BINDING 247 249 SUBSTRATE (BY SIMILARITY).
SQ SEQUENCE 302 AA; 32084 MW; B7D6550AAE88B4F4 CRC64;

BLAC_NOLIA Length: 302 March 17, 2003 12:16 Type: P Check: 8442 ..
Found using 'KTxs' (swope073.key)

197 RALAHDLRFYVLDGALAEDEDRALLTDLMLRRMTGGTVIRAGVPADWVVGDKTGGSGYGGYR
247

257 NDIAVIMPNRPIYMAVMTSREPRRAKADALLADARAVTA

1 match found in sequence:
blacprovu ; Beta-lactamase (EC 3.5.2.6) (Penicillinase).
(from "lactxs_sp.pep")
TOIG of: blac_provu check: 7122 from: 1 to: 271

ID BLAC_PROVU STANDARD; PRT; 271 AA.
AC P80298;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Beta-lactamase (EC 3.5.2.6) (Penicillinase).
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=585;
[1]

RP SEQUENCE.
RC STRAIN=RO104;
RX MEDLINE=94318667; PubMed=8043607;

RA Peduzzi J., Reynaud A., Barthelémy M., Baron P., Labia R.;

RT "Chromosomally encoded cephalosporin-hydrolyzing beta-lactamase of
Proteus vulgaris RO104 belongs to Ambler's class A.";

RL Biochim. Biophys. Acta 1207:31-39(1994).

CC -1- FUNCTION: HYDROLYSES BROAD-SPECTRUM BETA-LACTAM ANTIBIOTICS.

CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
amino acid.

CC -1- SUBUNIT: MONOMER.

CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.

CC HSSP: Q47066; 1BZA.

DR InterPro: IPR001466; Beta_lactamase.

DR InterPro: IPR000871; beta_lactamase_A.

DR Pfam: PF00144; beta-lactamase; 1.

DR PRINTS: PR00118; BLACTAMASEA.

DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.

KW Hydrolase; Antibiotic resistance.

FT ACT_SITE 46 46 BY SIMILARITY.

FT BINDING 210 212 SUBSTRATE (BY SIMILARITY).

SO SEQUENCE 271 AA; 29802 MW; C6148E4F2500DDDF CRC64;

BLAC_PROVU Length: 271 March 17, 2003 12:16 Type: P Check: 7122 ..
Found using 'KTxs' (swope073.key)

160 IMAKSIQALTLGDLGOSORQOLVTWLKGNNTGDSIKAGLPKHWIVGDKTGGDYGT
210

220 NDIAVIMPNRHPILIVVFTQCEODAKYRKDIIVKATEIVTKE

1 match found in sequence:
blacserfo ; Beta-lactamase (EC 3.5.2.6) (Penicillinase).

```

(from "lactxs-sp.pep")
TOIG of: blac_serfo check: 2946 from: 1 to: 267

ID BLAC_SERFO STANDARD; PRT; 267 AA.
AC P80545;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Beta-lactamase (EC 3.5.2.6) (Penicillinase).
OS Serratia fonticola.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia
CX NCBI_TaxID=47917;
RN [1]
RP SEQUENCE.
RC STRAIN-CUV;
RX MEDLINE=97444277; PubMed=9300809;
RA Peduzzi J., Farzaneh S., Reynaud A., Barthelémy M., Labia R.;
RT "Characterization and amino acid sequence analysis of a new oxyimino
RT cephalosporin-hydrolyzing class A beta-lactamase from Serratia
RT fonticola CUV."
RL Biochim. Biophys. Acta 1341:58-70(1997).
CC -1- FUNCTION: HYDROLYSES BROAD-SPECTRUM BETA-LACTAM ANTIBIOTICS.
CC ACTIVE AGAINST CEPHALOSPORINS.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- ENZYME REGULATION: INHIBITED BY CLAVULANIC ACID, SUBACTAM
CC AND TAZOBACTAM.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
DR HSSP; Q47066; 1BZA.
DR Interpro: IPR001466; Beta_lactamase.
DR Interpro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA-LACTAMASE_A; FALSE NEG.
KW Hydrolyase; Antibiotic resistance.
FT CHAIN 1 267 BETA-LACTAMASE, FORM I.
FT ACT_SITE 6 267 BETA-LACTAMASE, FORM II.
FT BINDING 49 49 BY SIMILARITY.
FT SEQUENCE 267 AA; 28754 MW; D70C1FDE63F09C3 CRC64;

BLAC_SERFO length: 267 March 17, 2003 12:16 Type: P Check: 2946 ..
Found using 'KTXS' (swope073.key)

...

163 QAMAI5LONLTGKALAPORALVEMWKGNTGASIRAGLPTTWVVGDKTSGDYGT 1--1
213

223 NDIAVIMFANHAPLVIVTYTFQPOQNMARADVLAATAKIYTAG

...

1 match found in sequence:
blacstr1 : Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).
(from "lactxs-sp.pep")
TOIG of: blac_stral check: 9207 from: 1 to: 314

ID BLAC_STRAL STANDARD; PRT; 314 AA.
AC P14559;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).
OS Streptomyces albus G.
OC Bacteria: Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
CX NCBI_TaxID=1962;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

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RX MEDLINE=87275916; PubMed=3038538;
RA Dehotay P., Dusart J., de Meester F., Joris B., van Beeumen J.,
RA Ericum T., Frere J.-M., Ghysen J.-M.;
RT "Nucleotide sequence of the gene encoding the Streptomyces albus G
RT beta-lactamase precursor."
RL Eur. J. Biochem. 166:345-350(1987).
RN [2]
RP SEQUENCE OF 81-92.
RX MEDLINE=88024011; PubMed=2822004;
RA de Meester F., Joris B., Lenzini M.V., Dehotay P., Ericum T.,
RA Dusart J., Klein D., Ghysen J.-M., Frere J.-M., van Beeumen J.;
RT "The active sites of the beta-lactamases of Streptomyces cacaoi and
RT Streptomyces albus G."
RL Biochem. J. 244:427-432(1987).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 47-314.
RA Fozze E., Charlier P., Dideberg O.;
RX Submitted (JUL-1998) to the PDB data bank.
RL -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC -----
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CC -----
DR EMBL; M28303; AAA26775.1; -.
DR PIR; S00057; PMSMU.
DR PDB; 1BSG; 13-JAN-99.
DR Interpro: IPR001466; Beta_lactamase.
DR Interpro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA-LACTAMASE_A; 1.
KW Hydrolyase; Antibiotic resistance; Signal; 3D-structure.
FT CHAIN 1 39 BETA-LACTAMASE.
FT ACT_SITE 40 314
FT BINDING 89 89
FT SEQUENCE 314 AA; 33265 MW; 5A17DD19C84E511 CRC64;

BLAC_STRAL length: 314 March 17, 2003 12:16 Type: P Check: 9207 ..
Found using 'KTXS' (swope073.key)

...

42 GSGSVDAERRLAGLRASGARLVYAYDTGSGRTVAYRADELFPWCVFKTLSSAAVL 1--1
92 95

102 DDDRNGEPLSRILTYDDVEQADGAGPETGKPNLANQLTVE

...

1 match found in sequence:
blacyeren : Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).
(from "lactxs-sp.pep")
TOIG of: blac_yeren check: 2339 from: 1 to: 294

ID BLAC_YEREN STANDARD; PRT; 294 AA.
AC Q00166;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).
OS Versinia enterocolitica.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;

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OC Versinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Y-56 / Serotype O:3;
RX MEDLINE=91360067; PubMed=1886608;
RA Seoane A., Garcia Lobo J.M.;
RT "Nucleotide sequence of a new class A beta-lactamase gene from the
  chromosome of Versinia enterocolitica: implications for the evolution
  of class A beta-lactamases."
RL Mol. Gen. Genet. 228:215-220(1991).
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O -> a substituted beta-
  amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC -----
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CC -----
CC EMBL: X57074; CAA40357.1; -.
CC PIR: S16553; S16553.
CC HSSP: Q47066; 1BZA.
DR InterPro: IPR001466; Beta_Lactamase.
DR InterPro: IPR000871; Beta_Lactamase_A.
DR Pfam: PF00144; beta-lactamase.1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolyase; Antibiotic resistance; Signal.
FT SIGNAL 1 30
FT CHAIN 1 294
FT ACT_SITE 75 75
FT BINDING 239 241
FT SEQUENCE 294 AA; 45E5B721A98B98C5 CRC64;
SQ
BLAST_YERN Length: 294 March 17, 2003 12:16 Type: P Check: 2339
Found using 'KTXS' (swope073.key)
...
189 AAMASMKLVVGDALRPAQRSQLAVWLKNTTGDAITRACAPTDWYGDGSGSDYGT
|---|
239
249 NDIAVLMPKAPIVLYVYFTOREKDAPRRDVLASVTKIILSQ
|---|
-----
1 match found in sequence:
blafmycfo ; Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).
(from "lacksx.sp.pep")
TOIG of: blaf_mycfo check: 5458 from: 1 to: 294
ID BLAF_MYCFO STANDARD; PRT; 294 AA.
AC Q59517;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Beta lactamase precursor (EC 3.5.2.6) (Penicillinase).
GN BLAF.
OS Mycobacterium fortuitum.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
  Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1766;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=94344037; PubMed=8065266;
RA Tamm J.C.S., Perilli M.G., Duez C., Trias J., Orefici G.,
  Fattorini L., Amicosante G., Oratore A., Joris B.,

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RT "Transcription and expression analysis, using lacZ and phoA gene
  fusions, of Mycobacterium fortuitum beta-lactamase genes cloned from
  a natural isolate and a high-level beta-lactamase producer."
RL Mol. Microbiol. 12:491-504(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RC STRAIN-D316;
RA Sauvage E., Fonce E., Vermeire M., Galleni M., Quinting B.,
  Frere J.-M., Charlier P.;
RT "The crystal structure of the class A beta-lactamase from
  Mycobacterium fortuitum: structural basis for a broad substrate
  specificity."
RL Submitted (SEP-1998) to the PDB data bank.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O -> a substituted beta-
  amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC -----
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CC -----
CC EMBL: L25634; AAA19882.1; -.
CC PDB: 1MFO; 23-SEP-98.
DR InterPro: IPR001466; beta_Lactamase.
DR InterPro: IPR000871; Beta_Lactamase_A.
DR Pfam: PF00144; beta-lactamase.1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolyase; Antibiotic resistance; Signal; 3D-structure.
FT SIGNAL 1 32
FT CHAIN 1 294
FT ACT_SITE 75 75
FT BINDING 237 239
FT VARIANT 82 82
FT VARIANT 116 116
FT SEQUENCE 294 AA; 30951 MW; 87DE5D633867B84 CRC64;
SQ
BLAF_MYCFO Length: 294 March 17, 2003 12:16 Type: P Check: 5458
Found using 'KTXS' (swope073.key)
...
187 TAAALAVGYRAILAGDALSPQRLGLEDMMRANOTSSMRAGLEGWTTADTKSGDYGST
|---|
237
247 NDAGIAPGPGQRLLYVMTRSAHDPKAKNRPILGELTALVY
|---|
-----
1 match found in sequence:
blanentcl ; Imipenem-hydrolysing beta-lactamase precursor (EC 3.5.2.6)
(from "lacksx.sp.pep")
TOIG of: blan_entcl check: 472 from: 1 to: 292
ID BLAN_ENTCL STANDARD; PRT; 292 AA.
AC P52663;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Imipenem-hydrolysing beta-lactamase precursor (EC 3.5.2.6)
  (Carbapenemase) (NMC-A).
GN NMCA.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
  Enterobacter.
OX NCBI_TaxID=550;
RN [1]

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RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-34.
RC STRAIN-NOR-1;
RX MEDLINE=94329582; PubMed=8052644;
RA Naas T., Nordmann P.;
RT "Analysis of a carbapenem-hydrolyzing class A beta-lactamase from
  Enterobacter cloacae and of its LysR-type regulatory protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:7693-7697(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.89 ANGSTROMS).
RC STRAIN-NOR-1;
RX MEDLINE=93935084; PubMed=10464248;
RA Mouley L., Kotra L.P., Belletini J., Bulychew A., O'Brien M.,
  Miller M.J., Mobashery S., Samama J.-P.;
RT "Inhibition of the broad spectrum nonmetallocarbapenemase of class A
  beta-lactams.";
RL J. Biol. Chem. 274:25260-25265(1999).
CC -1- FUNCTION: HYDROLYSES CARBAPENEMS SUCH AS IMIPENEM, WHICH ARE
  EXTENDED-SPECTRUM BETA-LACTAM ANTIBIOTICS.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
  amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC -----
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CC -----
CC EMBL; Z21956; CA79967.1; -.
CC PDB; 1BUL; 30-DEC-98.
CC InterPro: IPR001466; Beta_lactamase.
CC InterPro: IPR000871; Beta_lactamase_A.
CC Pfam: PF00144; beta_lactamase; 1.
CC PRINTS; PR00118; BLACTAMASEA.
CC PROSITE; PS00146; BETA_LACTAMASE_A; FALSE_NEG.
CC KMW Hydrolyase; Antibiotic resistance; Signal; 3D-structure.
CC FT SIGNAL 1 27
CC CHAIN 1 292 IMIPENEM-HYDROLYSING BETA-LACTAMASE.
CC FT ACT_SITE 71 71 BY SIMILARITY.
CC FT BINDING 236 238 SUBSTRATE (BY SIMILARITY).
CC FT DISULFID 70 240
CC SQ SEQUENCE 292 AA; 32075 MW; 4D33FD866998F1B CRC64;

BLAN ENCL length: 292 March 17, 2003 12:16 Type: P Check: 472
Found using 'ktxs' (swope073.key)

...

186 AAVAKSLTKLALGNLSEHEKETQYTWLKGNTTGARIRASVPDWDVGDGSGCAYGT 1--1
236

246 ANDYAVWPKNRAPLLISVYTTKNEKAKHEDKVIASRIAD

```

2 matches found in sequence:
 blanserna; Carbapenem-hydrolyzing beta-lactamase Sme-1 precursor (EC 3.5.2.6)
 (from "ktxs_sp.pep")

TOIG of: blan_serma check: 7397 from: 1 to: 294

```

ID BLAN_SERMA STANDARD: PRT; 294 AA.
AC P52682;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Carbapenem-hydrolyzing beta-lactamase Sme-1 precursor (EC 3.5.2.6).
GN SmeA OR BpL-1.
OS Serratia marcescens.

```

```

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-38.
RC STRAIN-S6;
RX MEDLINE=94379777; PubMed=8092824;
RA Naas T., Vandel L., Sougakoff W., Livermore D.M., Nordmann P.;
RT "Cloning and sequence analysis of the gene for a
  carbapenem-hydrolyzing class A beta-lactamase, Sme-1, from Serratia
  marcescens S6.";
RL Antimicrob. Agents Chemother. 38:1262-1270(1994).
RN [2]
RP SEQUENCE OF 1-32 FROM N.A.
RC STRAIN-S6;
RX MEDLINE=95314194; PubMed=7793864;
RA Naas T., Livermore D.M., Nordmann P.;
RT "Characterization of an LysR family protein, Smer from Serratia
  marcescens S6, its effect on expression of the carbapenem-hydrolyzing
  beta-lactamase Sme-1, and comparison of this regulator with other
  beta-lactamase regulators.";
RL Antimicrob. Agents Chemother. 39:629-637(1995).
CC -1- FUNCTION: CAN HYDROLYZE CARBAPENEM COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
  amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC -----
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CC -----
CC EMBL; Z28968; CA82281.1; -.
CC DR EMBL; Z30237; CA82944.1; -.
CC DR HSSP; P52663; 1BUL.
CC DR InterPro: IPR001466; Beta_lactamase.
CC DR InterPro: IPR000871; Beta_lactamase_A.
CC Pfam: PF00144; beta_lactamase; 1.
CC PRINTS; PR00118; BLACTAMASEA.
CC PROSITE; PS00146; BETA_LACTAMASE_A; FALSE_NEG.
CC KMW Hydrolyase; Antibiotic resistance; Signal.
CC FT SIGNAL 1 27
CC CHAIN 1 294 CARBAPENEM-HYDROLYSING BETA-LACTAMASE
CC FT ACT_SITE 73 73 BY SIMILARITY.
CC FT BINDING 238 240 SUBSTRATE (BY SIMILARITY).
CC SQ SEQUENCE 294 AA; 32196 MW; C33AAD6AA2293094 CRC64;

BLAN SERMA length: 294 March 17, 2003 12:16 Type: P Check: 7397
Found using 'ktxs' (swope073.key)

...

1 MSNRKVFETKTSFLFVCLALSAFNHANKSDAAAKQIKLEEDFDGRIGVFAIDTGSNT 1--1
8 11

61 F

188 KAVANSLNKLALGNVLNAKVKATLYQWLKGNNTGDRIRASVPADWDVGDGSGCALGT 1--1
238

248 ANDYAVIWPKNRAPLLISVYTTKRSKDKXSDKTIAESRIAD

```

1 match found in sequence:
 blcicoll; Beta-lactamase CTX-M-1 precursor (EC 3.5.2.6) (Cefotaximase 1) (ME

(from "lactxs_sp.pep")
TOIG of: b1c1_ecoli check: 1321 from: 1 to: 291

ID B1C1_ECOLI STANDARD; PRT; 291 AA.
AC P28585;
DT 01-DEC-1992 (Rel. 24, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-lactamase CTX-M-1 precursor (EC 3.5.2.6) (Cefotaximase 1) (MEN-1).
GN BLA OR MEN1.
OS Escherichia coli.
OC Plasmid pMVP-3.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GRI-1;
RX MEDLINE=96431831; PubMed=8834913;
RA Baerentzen A., Stempling I., Jungwirth R., Casellas J.M.;
RT "Sequences of beta-lactamase genes encoding CTX-M-1 (MEN-1) and CTX-M-2 and relationship of their amino acid sequences with those of other beta-lactamases";
RT Antimicrob. Agents Chemother. 40:509-513(1996).
RN [2]
RP SEQUENCE OF 29-291.
RC STRAIN-MEN;
RX MEDLINE=92338218; PubMed=1633193;
RA Barthelemy M., Peduzzi J., Bernard H., Tancredi C., Labia R.;
RT "Close amino acid sequence relationship between the new plasmid-mediated extended-spectrum beta-lactamase MEN-1 and chromosomally encoded enzymes of Klebsiella oxyloca";
RT Biochim. Biophys. Acta 1122:15-22(1992).
CC -1- FUNCTION: BROAD SPECTRUM BETA-LACTAMASE WHICH CONFERES RESISTANCE TO PENICILLINS, AS WELL AS FIRST, SECOND AND THIRD-GENERATION CEPHALOSPORINS.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
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CC -----
DR EMBL: X92506; CA63262.1; -.
DR PIR: S23929; S23929.
DR HSP: Q47066; IBZA.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolase; Antibiotic resistance; Plasmid; Signal.
FT CHAIN 1 28
FT ACT_SITE 29 291 BETA-LACTAMASE CTX-M-1.
FT BINDING 73 73 BY SIMILARITY.
FT BINDING 237 239 SUBSTRATE (BY SIMILARITY).
SQ SEQUENCE 291 AA; 31245 MW; D82501CF8AE5FC5 CRC64;

BLC1_ECOLI Length: 291 March 17, 2003 12:16 Type: P Check: 1321 ..
Found using 'KTXS' (swope073.key)

187 RAMAQTIRNLTKALGDSORAOVLTWKGNTTGASTIOAGLIPASWVGDKTSGSDYGT 1--1
237

247 NDIAVIMPKDRAPLIVTYFTPOPKAESRRDVLASAKITVNG
.....
1 match found in sequence:
b1c2salty; Beta-lactamase CTX-M-2 precursor (EC 3.5.2.6) (Cefotaximase 2).
(from "lactxs_sp.pep")
TOIG of: b1c2_salty check: 7862 from: 1 to: 291

ID B1C2_SALTY STANDARD; PRT; 291 AA.
AC P74841;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-lactamase CTX-M-2 precursor (EC 3.5.2.6) (Cefotaximase 2).
GN Salmonella typhimurium.
OS Plasmid pMVP-4.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAS-5;
RX MEDLINE=96431831; PubMed=8834913;
RA Baerentzen A., Stempling I., Jungwirth R., Casellas J.M.;
RT "Sequences of beta-lactamase genes encoding CTX-M-1 (MEN-1) and CTX-M-2 and relationship of their amino acid sequences with those of other beta-lactamases";
RT Antimicrob. Agents Chemother. 40:509-513(1996).
CC -1- FUNCTION: HAS CEFOTAXIME-HYDROLYZING ACTIVITY.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
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CC -----
DR EMBL: X92507; CA63263.1; -.
DR HSP: Q47066; IBZA.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolase; Antibiotic resistance; Plasmid; Signal.
FT CHAIN 1 28
FT ACT_SITE 29 291 BETA-LACTAMASE CTX-M-2.
FT BINDING 73 73 BY SIMILARITY.
FT BINDING 237 239 SUBSTRATE (BY SIMILARITY).
SQ SEQUENCE 291 AA; 31377 MW; 82277CD9CDA1E7C0 CRC64;

BLC2_SALTY Length: 291 March 17, 2003 12:16 Type: P Check: 7862 ..
Found using 'KTXS' (swope073.key)

187 LAMAQTIRNLTKALAEOTORAOVLTWKGNTTGASIRAGLEKRSWVGDKTSGSDYGT 1--1
237

247 NDIAVIMPKDRAPLIVTYFTPOPKAESRRDVLAAAKIVTHG

1 match found in sequence:

```

b1c3salty; Beta-lactamase CTX-M-3 precursor (EC 3.5.2.6) (Cefotaximase 3).
(from "lacks_sp.pep")
TOIG of: b1c3_salty check: 8071 from: 1 to: 291

ID B1C3_SALTY STANDARD; PRT; 291 AA.
AC O33807;
DC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-lactamase CTX-M-3 precursor (EC 3.5.2.6) (Cefotaximase 3).
GN BLA.
OS Salmonella typhimurium.
OC Plasmid pAS31.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RA Gazouli M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: HAS CEFOTAXIME-HYDROLYZING ACTIVITY.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Y14156; CAA74573.1; -.
CC HSSP: Q47066; 1BZA.
CC InterPro: IPR001466; Beta_lactamase.
CC InterPro: IPR000871; Beta_lactamase_A.
CC Pfam: PF00144; beta-lactamase; 1.
CC PRINTS: PR00118; BLACTAMASEA.
CC PROSITE: PS00146; BETA_LACTAMASE_A; 1.
CC Hydrolyase; Antibiotic resistance; Plasmid; Signal.
CC CHAIN 1 28
CC SIGNAL 1 28
CC FT CHAIN 29 291 BETA-LACTAMASE CTX-M-3.
CC FT ACT_SITE 73 73 BY SIMILARITY.
CC FT BINDING 237 239 SUBSTRATE (BY SIMILARITY).
CC SQ SEQUENCE 291 AA; 31254 MW; 2E22E251008DFC6 CRC64;

B1C3_SALTY length: 291 March 17, 2003 12:16 Type: P Check: 8071 ..
Found using 'ktxs' (swope073.key)

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OS Salmonella typhimurium.
OG Plasmid pAS30.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RA Gazouli M.; Tzelepi E., Markogiannakis A., Legakis N., Tzouveleakis L.;
RL "Two novel plasmid-mediated cefotaxime-hydrolyzing beta-lactamases
(RT CTX-M-5 and CTX-M-6) from Salmonella typhimurium";
Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: HAS CEFOTAXIME-HYDROLYZING ACTIVITY.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ005044; CAA06311.1; -.
CC HSSP: Q47066; 1BZA.
CC InterPro: IPR001466; Beta_lactamase.
CC InterPro: IPR000871; Beta_lactamase_A.
CC Pfam: PF00144; beta-lactamase; 1.
CC PRINTS: PR00118; BLACTAMASEA.
CC PROSITE: PS00146; BETA_LACTAMASE_A; 1.
CC Hydrolyase; Antibiotic resistance; Plasmid; Signal.
CC CHAIN 1 28
CC SIGNAL 1 28
CC FT CHAIN 29 291 BETA-LACTAMASE CTX-M-5.
CC FT ACT_SITE 73 73 BY SIMILARITY.
CC FT BINDING 237 239 SUBSTRATE (BY SIMILARITY).
CC SQ SEQUENCE 291 AA; 31251 MW; DC01C3F73789894E CRC64;

B1C5_SALTY length: 291 March 17, 2003 12:16 Type: P Check: 8066 ..
Found using 'ktxs' (swope073.key)

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187 LAMAQTLKNTLTKALAEFQRAQLVTWIKGNTGASIRAGMKSGVGDGTSGDYGT
1--1
237

247 NDIAVWPENHAPLVVITYFTPEOKAESRRDILAAAKIVTHG

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1 match found in sequence:
b1c6salty; Beta-lactamase CTX-M-6 precursor (EC 3.5.2.6) (Cefotaximase 6).
(from "lacks_sp.pep")
TOIG of: b1c6_salty check: 8537 from: 1 to: 291

ID B1C6_SALTY STANDARD; PRT; 291 AA.
AC O65976;
DC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-lactamase CTX-M-6 precursor (EC 3.5.2.6) (Cefotaximase 6).
GN BLA.
OS Salmonella typhimurium.
OG Plasmid pAS31.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AS31;

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RA  Gazouli M., Tzelepi E., Markogiannakis A., Legakis N., Tzouveleakis L.;
RT  "Two novel plasmid-mediated cefotaxime-hydrolyzing beta-lactamases
RT  (CTX-M-5 and CTX-M-6) from Salmonella typhimurium.";
RL  Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
CC  -1- FUNCTION: HAS CEFOTAXIME-HYDROLYZING ACTIVITY.
CC  -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC  amino acid.
CC  -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AJ005045; CA06312.1; -.
DR  HSSP; Q47066; 1BZA.
DR  InterPro: IPR001466; Beta_lactamase.
DR  InterPro: IPR000871; Beta_lactamase_A.
DR  Pfam; PF00144; beta_lactamase; 1.
DR  PRINTS; PR00118; BLACTAMASEA.
DR  PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW  Hydrolase; Antibiotic resistance; Plasmid; Signal.
FT  SIGNAL 1 28 BY SIMILARITY.
FT  CHAIN 29 291 BETA-LACTAMASE CTX-M-6.
FT  ACT_SITE 73 73 BY SIMILARITY.
FT  BINDING 237 239 SUBSTRATE (BY SIMILARITY).
SQ  SEQUENCE 291 AA: 31206 MW; DC95E4FE7531053 CRC64;
BL06_SALTY Length: 291 March 17, 2003 12:16 Type: P Check: 8537
Found using 'KTXS' (swope073.key)
...
187 LAMAQTLKNLTLGKALAEQRAQVLTWLGKNTGSGASIRAGLPKSGVGDGTSGDGYTT 1--1
237
247 NDIAVTPENHAPLVLTFTYFQPEQKAESRDVLAANKIVTHG
...
1 match found in sequence:
blt1ecoli; Beta-lactamase Toho-1 precursor (EC 3.5.2.6).
(from "lactxs_sp.pep")
TOIG of: blt1_ecoli check: 7815 from: 1 to: 291
ID BLT1_ECOLI STANDARD; PRT; 291 AA.
AC 047066;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-lactamase Toho-1 precursor (EC 3.5.2.6).
GN BLA.
OS Escherichia coli.
OC Plasmid.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TUHI12191;
RX MEDLINE=96109425; PubMed=8619581;
RA Ishii Y., Ohno A., Taguchi H., Imajo S., Ishiguro M., Matsuzawa H.;
RT "Cloning and sequence of the gene encoding a cefotaxime-hydrolyzing
RT class A beta-lactamase isolated from Escherichia coli.";
RL Antimicrob. Agents Chemother. 39:2269-2275(1995).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT ALA-169.
RC STRAIN-TUHI12191;

```

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FX MEDLINE=99126537; PubMed=9925786;
RA Iibuka A., Taguchi A., Ishiguro M., Fushinobu S., Ishii Y.,
RA Kanitori S., Okuyama K., Yamaguchi K., Kono M., Matsuzawa H.;
RT "Crystal structure of the E166A mutant of extended-spectrum
RT beta-lactamase Toho-1 at 1.8 A resolution.";
RL J. Mol. Biol. 285:2079-2087(1999).
CC -1- FUNCTION: HAS STRONG CEFOTAXIME-HYDROLYZING ACTIVITY.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; D37830; BAA07082.1; -.
DR  PDB; 1BZA; 27-APR-99.
DR  InterPro: IPR001466; Beta_lactamase.
DR  InterPro: IPR000871; Beta_lactamase_A.
DR  Pfam; PF00144; beta_lactamase; 1.
DR  PRINTS; PR00118; BLACTAMASEA.
DR  PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW  Hydrolase; Antibiotic resistance; Signal; Plasmid; 3D-structure.
FT  SIGNAL 1 29 BY SIMILARITY.
FT  CHAIN 30 291 BETA-LACTAMASE TOHO-1.
FT  ACT_SITE 73 73
FT  BINDING 237 239 SUBSTRATE.
SQ  SEQUENCE 291 AA: 31447 MW; 83FC0C9CD41E7C0 CRC64;
BLT1_ECOLI Length: 291 March 17, 2003 12:16 Type: P Check: 7815
Found using 'KTXS' (swope073.key)
...
187 LAMAQTLKNLTLGKALAEQRAQVLTWLGKNTGSGASIRAGLPKSGVGDGTSGDGYTT 1--1
237
247 NDIAVTPENHAPLVLTFTYFQPEQKAERRDLIAANKIVTHG
...
1 match found in sequence:
blt2ecoli; Beta-lactamase Toho-2 precursor (EC 3.5.2.6).
(from "lactxs_sp.pep")
TOIG of: blt2_ecoli check: 7692 from: 1 to: 289
ID BLT2_ECOLI STANDARD; PRT; 289 AA.
AC 069395;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-lactamase Toho-2 precursor (EC 3.5.2.6).
GN BLA.
OS Escherichia coli.
OC Plasmid IncFII PMY036.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TUM1083;
RX MEDLINE=98253979; PubMed=9593147;
RA Ma L., Ishii Y., Ishiguro M., Matsuzawa H., Yamaguchi K.;
RT "Cloning and sequencing of the gene encoding Toho-2, a class A beta-
RT lactamase preferentially inhibited by tazobactam.";
RL Antimicrob. Agents Chemother. 42:1181-1186(1998).

```

CC -1- FUNCTION: HYDROLYSES BETA-LACTAM ANTIBIOTICS SUCH AS PENICILLIN G,
 CC CARBENICILLIN, CEPHALORIDINE, CEFOTAXIME, CEFOTAZIDIME,
 CC AND AZTREONAM. HAS ESPECIALLY INCREASED RELATIVE HYDROLYSIS RATES
 CC FOR CEPHALORIDINE, CEFOTAXIME, AND CEFOTIZOXIME.
 CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 CC amino acid.
 CC -1- ENZYME REGULATION: INHIBITED 16-FOLD BETTER BY THE BETA-LACTAMASE
 CC INHIBITOR TAZOBACTAM THAN BY CLAVULANIC ACID.
 CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; D89862; BAA28282.1; -
 CC DR HSSP; Q47066; LBZA.
 CC DR InterPro; IPR001466; Beta_Lactamase.
 CC DR InterPro; IPR000871; Beta_Lactamase_A.
 CC DR Pfam; PF00144; beta-lactamase; 1.
 CC DR PROSITE; PS00146; BETA-LACTAMASE_A; 1.
 CC KW Hydrolyase; Antibiotic resistance; Signal; Plasmid.
 CC FT SIGNAL 1 28 POTENTIAL.
 CC FT CHAIN 29 289 BETA-LACTAMASE TOHO-2.
 CC FT ACT_SITE 73 73 BY SIMILARITY.
 CC FT BINDING 235 237 SUBSTRATE (BY SIMILARITY).
 CC FT SEQUENCE 289 AA; 30745 MW; A75723E1793060A6 CRC64;
 CC SQ
 CC BLT2_ECOLI length: 289 March 17, 2003 12:16 Type: P Check: 7692 ..
 CC Found using 'KTXS' (swope073.key)

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azeredo V., Bertero M.G., Bessieres P., Bolotin A., Borcher S.,
 RA Borriss R., Bourrier L., Brans A., Braun M., Brigell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuno V., Carter N.M.,
 RA Choi S.K., Codan J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine J.M., Distenhof A., Ehrlich S.D., Emerson P.T.,
 RA Ertlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritze C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Kleier-Blanchard M., Klein C.,
 RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Yamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Wetzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zanchin A.;
 RA "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RA subtilis".
 RA Nature 390:249-256(1997).
 RA [3]
 RA SEQUENCE OF 32-102.
 RA MEDLINE=80182289; PubMed=6768745;
 RA Waxman D.J., Strominger J.L.;
 RA "Sequence of active site peptides from the penicillin-sensitive D-
 RA alanine carboxypeptidase of *Bacillus subtilis*. Mechanism of
 RA penicillin action and sequence homology to beta-lactamases.";
 RA J. Biol. Chem. 255:3964-3976(1980).
 RA [4]
 RA SEQUENCE OF 103-443 FROM N.A.
 RA MEDLINE=86250602; PubMed=3087956;
 RA Todd J.A., Roberts A.N., Johnstone K., Pigot P.J., Winter G.,
 RA Ellar D.J.;
 RA "Reduced heat resistance of mutant spores after cloning and
 RA mutagenesis of the *Bacillus subtilis* gene encoding penicillin-binding
 RA protein 5.";
 RA J. Bacteriol. 167:257-264(1986).
 RA [5]
 RA SEQUENCE OF 414-443.
 RA MEDLINE=81117303; PubMed=6780559;
 RA Waxman D.J., Strominger J.L.;
 RA "Primary structure of the COOH-terminal membranous segment of a
 RA penicillin-sensitive enzyme purified from two *Bacillus*.";
 RA J. Biol. Chem. 256:2067-2077(1981).
 CC -1- FUNCTION: REMOVES C-TERMINAL D-ALANYL RESIDUES FROM SUGAR-PEPTIDE
 CC CELL WALL PRECURSORS.
 CC -1- CATALYTIC ACTIVITY: D-alanyl-D-alanine + H(2)O = 2 D-alanine.
 CC -1- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S11; ALSO KNOWN AS THE
 CC D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 1 FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; D26185; BAA05246.1; -
 CC EMBL; Z99104; CAB11786.1; -


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DR EMBL: M13766; AAA22375.1;
DR PIR: A23307; A23307.
DR MEROPS: S11.001; -.
DR Subtilisin; BGI0074; dact.
DR InterPro: IPR001967; Ala/AlaCpTase1.
DR Pfam: PF00768; Peptidase_S11; 1.
DR PRINTS: PR00725; DADACBPTASE1.
KW Hydrolase; Carboxypeptidase; Peptidoglycan synthesis; Cell wall;
KW Membrane; Signal; Complete proteome.
FT SIGNAL 1 31
FT CHAIN 32 443 D-ALANYL-D-ALANINE CARBOXYPEPTIDASE.
FT ACT_SITE 67 67 ACYLATED BY PENICILLIN.
FT CONFLICT 100 100 E -> Q (IN REF. 3).
FT CONFLICT 227 227 E -> Q (IN REF. 4).
SQ SEQUENCE 443 AA: 48636 MW: DA6C5B0307DC117 CRC64;
DACA_BACSU Length: 443 March 17, 2003 12:16 Type: P Check: 4418
Found using 'KTXS' (swope073.key)

208 ITDYEILLETSSIAKTFREGTDEMDMPNMNMLKGLVSEKKATVDGLTGSTDSAGS
258
268 CFTGTAERNGMVITVVLNANGNLHTGRFDETKKMFQAFDNFSMKETIYAGSDVKGKHT
326
328 ISVDGKEKEVGIYTKAFSLPVKNGEENKAKVATLKNKMLTAIPVKKGTKY
329

1 match found in sequence:
ppb4ecoli; Penicillin-binding protein 4 precursor (PBP-4) [Includes: D-alanyl-
(from "lactix_sp.pep")
TOIG of: ppb4_ecoli check: 5942 from: 1 to: 477

ID PBP4_ECOLI STANDARD; PRT; 477 AA.
AC P24228;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Penicillin-binding protein 4 precursor (PBP-4) [Includes: D-alanyl-D-
alanine carboxypeptidase (EC 3.4.16.4) (DD-peptidase) (DD-
carboxypeptidase); D-alanyl-D-alanine-endopeptidase (EC 3.4.99.-) (DD-
endopeptidase)].
DE DADB OR B3182.
GN DADB OR B3182.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-31.
RC STRAIN=K12 / W3110;
RX MEDLINE=91250093; PubMed=2040429;
RA Motil H., Terpstra P., Keck W.;
RT "Penicillin-binding protein 4 of Escherichia coli shows a novel type
of primary structure among penicillin-interacting proteins.";
RL FEWS Microbiol. Lett. 62:213-220(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Wang R., Kushner S.R.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / M61655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

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RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=91260452; PubMed=2046551;
RA Korat B., Motil H., Keck W.;
RT "Penicillin-binding protein 4 of Escherichia coli: molecular cloning
of the dact gene, controlled overexpression, and alterations in
murein composition."
RL Mol. Microbiol. 5:675-684(1991).
CC -1- FUNCTION: NOT INVOLVED IN TRANSEPTIDATION BUT EXCLUSIVELY
CATALYZES A DD-CARBOXYPEPTIDASE AND DD-ENDOPEPTIDASE REACTION.
CC -1- CATALYTIC ACTIVITY: D-alanyl-D-alanine + H(2)O = 2 D-alanine.
CC -1- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC -1- MISCELLANEOUS: IN E. COLI THERE ARE THREE MUREIN ENDOPEPTIDASES:
CC TWO ARE PENICILLIN SENSITIVE (PBP4 AND PBP7), THE OTHER (MEPA)
CC NOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S13; ALSO KNOWN AS THE
CC D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 3 FAMILY.
CC
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CC
DR EMBL: X59460; CA42070.1; -.
DR EMBL: X60038; CA44264.1; -.
DR EMBL: U01376; AAA97505.1; -.
DR EMBL: U18997; AAA57983.1; -.
DR EMBL: AE000399; AAC76214.1; -.
DR MEROPS: S13.001; -.
DR Ecogen: EGI0202; dact.
DR InterPro: IPR000667; Peptidase_S13.
DR Pfam: PF02113; Peptidase_S13; 1.
DR PRINTS: PR00922; DADACBPTASE3.
DR TIGRFAMs: TIGR00666; PBP4_1.
KW Peptidoglycan synthesis; Cell division; Cell wall; Hydrolase; Signal;
KW Antibiotic resistance; Periplasmic; Complete proteome.
FT SIGNAL 1 20
FT CHAIN 21 477
FT ACT_SITE 62 62
FT ACT_SITE 417 417
FT DOMAIN 90 263
FT CONFLICT 427 427 L -> Q (IN REF. 1; CA442643).
SQ SEQUENCE 477 AA: 51798 MW: 4EF5E43D2BC4E5B CRC64;

PBP4_ECOLI Length: 477 March 17, 2003 12:16 Type: P Check: 5942
Found using 'KTXS' (swope073.key)

367 PATMQVLYQYIAQHDELNFIISMLPLAGYDGLQYRAGLHQAGVDKYSAGKTSGLGYVN
417
427 LAGFITTAGSGORMAFVOYLSGVAVEPADQRNRRIPLVRESRLY
417

1 match found in sequence:
tpnabactr; Transposase for insertion sequence element IS21-like.
(from "lactix_sp.pep")
TOIG of: tnpa_bactr check: 299 from: 1 to: 582

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ID  TNPA_BACFR      STANDARD;      PRT;      582 AA.
AC  Q45119;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Transposase for insertion sequence element IS21-like.
GN  TNPA.
OS  Bacteroides fragilis.
OC  Bacteria; Bacteroidetes; Bacteroides; Bacteroidales; Bacteroidaceae;
OC  Bacteroides.
OX  NCBI_TaxID=817;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=REF-103;
RX  MEDLINE=94292468; PubMed=7517394;
RA  Rogers M.B., Bennett T.K., Payne C.M., Smith C.J.;
RT  "Insertional activation of cepA leads to high-level beta-lactamase
RT  expression in Bacteroides fragilis clinical isolates.";
RL  J. Bacteriol. 176:4376-4384(1994).
CC  -1- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION
CC  SEQUENCE (POTENTIAL).
CC  -1- SIMILARITY: BELONGS TO THE IS21/IS408/IS1162 FAMILY OF
CC  TRANSPOSASES.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: U05888; AAA21540.1; -.
DR  InterPro: IPR001584; Rve.
DR  Pfam: PF00665; Ive; 1.
KW  Transposable element; Transposition; DNA-binding; DNA recombination.
SQ  SEQUENCE 582 AA; 68998 MW; FD01D8DEA67D1A07 CRC64;

TNPA_BACFR Length: 582 March 17, 2003 12:16 Type: P Check: 299 ..
Found using 'KTXS' (swope073.key)

1  MIHGHILLIRLDRFHLFHRIVDCNFTSGTSHRSHFYRGIMFLPCGNVYLCLNKETD 1--1
30 33

61  TGMETKSONLKDRLYMKVREL

-----
1 match found in sequence:
yc36metja: Hypothetical protein MJ1236.
(from 'ktxs_sp.pep')
TOIG of: yc36_metja check: 4523 from: 1 to: 634

ID  YC36_METJA      STANDARD;      PRT;      634 AA.
AC  Q58633;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Hypothetical protein MJ1236.
GN  MJ1236.
OS  Methanococcus jannaschii.
OC  Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC  Methanocaldococcaceae; Methanocaldococcus.
OX  NCBI_TaxID=2190;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX  MEDLINE=96337999; PubMed=8688087;
RA  Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA  Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA  Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

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RA  Overbeek R., Kirkness E.F., Weinstein K.G., Merrick J.M., Glodok A.,
RA  Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA  Uttenback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA  Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA  Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.;
RT  "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT  jannaschii.";
RL  Science 273:1058-1073(1996).
CC  -1- SIMILARITY: STRONG TO M.JANNASCHII MJ0047 AND MJ0162. ALSO
CC  SIMILAR TO SYNECHOCYSTIS PCC 6803 SLI0514.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: U67564; AAB99240.1; -.
DR  TIGR: MJ1236; -.
DR  InterPro: IPR001279; Bactamase-like.
DR  InterPro: IPR004087; KH_dom.
DR  Pfam: PF00013; KH-domain; 1.
DR  Pfam: PF00753; lactamase_B; 1.
DR  SMART: SM00322; KH; 1.
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 634 AA; 71760 MW; F6FB9D6C07732A15 CRC64;

YC36_METJA Length: 634 March 17, 2003 12:16 Type: P Check: 4523 ..
Found using 'KTXS' (swope073.key)

508  LTGSPVEYLKHLAPDEKNALIFVGVAEGTLGRKVGSGMKRPIITRNGKTKSIPINLQ 1--1
558

568  VYIEGSGHSDRKQLIKYIRLRKPSPEKIIWVHGSESKLDFEA

-----
-- Search Statistics --
Times:          CPU          Total Elapsed
00:00:00.02     00:00:02.00

Number of sequences searched: 30
Number of sequence hits: 30
Number of separate matches: 33
Number of sequence hits saved: 0

```

> 0 <
0110 IntelliGenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "ktxs_spt" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence: "swope073.key":

Selected sequence key from "ktxs_aa preliminary pattern"

KTxs (AA) ID KTxs AA preliminary pattern

1 followed by

2 kt

2 any character

Selected files:

File : laktxs_spt.pep

-- Output Parameters --

Format Options:	File Options:
Nucleic acid code matching	Exact
Find non-matching hits only	Indirect file
Report key used	Sequence or key file
Note position of hit	List of hits
Display full annotations	Hit display
Sequence context	Name and annotations

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

1 match found in sequence:

008498 ; Beta-lactamase (EC 3.5.2.6) (Penicillinase) (Cephalosporinase) (Class
from "laktxs_spt.pep")
TOIG of: 008498 check: 3751 from: 1 to: 249

ID 008498 PRELIMINARY; PRT; 249 AA.
AC 008498;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Beta-lactamase (EC 3.5.2.6) (Penicillinase) (Cephalosporinase) (Class
B CARBAPEMASE BLAB-1).
GN BLAB.
OS Flavobacterium meningosepticum.
OC Bacteria: CFB group; Flavobacteriia; Flavobacteriaceae;
CC Chryseobacterium.
OX NCBI_TaxID=238;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCUG4310;
RA Rossolini G.M., Riccio M.L., Lombardi G., Thaller M.C., Amicosante G.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PINT;
RA MEDLINE=20316804; PubMed=10858348;
RA Bellais S., Aubert D., Naas T., Nordmann P.;
RT "Molecular and biochemical heterogeneity of class B carbapenem-
hydrolyzing beta-lactamases in Chryseobacterium meningosepticum.";
RL Antimicrob. Agents Chemother. 44:1878-1886(2000).
CC -I- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2O) = A SUBSTITUTED BETA-
AMINO ACID.
CC -I- COFACTOR: ZINC (IN CLASS-B ENZYMES).

DR EMBL; X96858; CA65601.1; -.
DR EMBL; AF189298; AAF89154.1; -.
DR HSSP; P04190; 2BC2.
DR InterPro: IPR001018; Beta_lactamase_B.
DR InterPro: IPR001279; Bactamase-like.
DR Pfam; PF00753; Lactamase_B; 1.
DR ProDom; PD007656; Beta_lactamase_B; 1.
DR PROSITE; PS00744; BETA_LACTAMASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 249 AA; 28144 MW; 0F042B5126E338F6 CRC64;

008498 Length: 249 March 17, 2003 12:32 Type: P Check: 3751
Found using 'KTxs' (swope073.key)

66 VIDCPMGEDKFKSPTDEIYKKGKRYIMNIA7SHDDRAGGLEFGKIGAKTSTKMTDS
116

126 ILAKENPRAQYTFDNNKSPKVGKSEFQVYYPGKGHTADNVVW

1 match found in sequence:

015766 ; Heat-shock cognate protein 70.
(from "laktxs_spt.pep")
TOIG of: 015766 check: 8263 from: 1 to: 632

ID 015766 PRELIMINARY; PRT; 632 AA.
AC 015766;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, last annotation update)
DE Heat-shock cognate protein 70.
GN HSC70.
OS Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RA Boyes H., Mintert U., Dittlich W., Faix J., Gerisch G.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; AF025951; AAB81865.1; -.
DR HSSP; P19120; 3HSC.
DR InterPro: IPR000871; Beta_lactamase_A.
DR InterPro: IPR001023; Hsp70.
DR InterPro: IPR00169; Shpitol_acsite.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; HSP70; 1.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
KW ATP-binding.
SQ SEQUENCE 632 AA; 69799 MW; 33E142E2B40607C9 CRC64;

015766 Length: 632 March 17, 2003 12:32 Type: P Check: 8263
Found using 'KTxs' (swope073.key)

61 PTNTIFDAKRLIKGKSDPVYQSDMKHWPVKVIAKEGDKPHLOVEFGKVKTSPEVSS
111

121 MYLKMKEFAEAYLGKTTINNAVITVPAYFNDQROATKAGAI

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...
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1 match found in sequence:
024684 ; Bla LAF-3 (Fragment).
(from "lactxs_spt.pep")
TOIG of: 024684 check: 557 from: 1 to: 381

ID 024684 PRELIMINARY; PRT; 381 AA.
AC 024684:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Bla LAF-3 (Fragment).
GN APC.
OS Salmonella sentfenberg.
OC Plasmid pSENf.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmomella.
OX NCBI_TaxID=28150;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SENF;
RX MEDLINE-97375066; PubMed-9231418;
RA Koeck J.L., Arlet G., Philippson A., Basmaciogullari S., Then H.V.,
RA Bulsson Y., Cavallo J.D.;
RT "A plasmid-mediated CMY-2 beta-lactamase from an Algerian clinical
RT isolate of salmonella sentfenberg.";
RL FEMS Microbiol. Lett. 152:255-260(1997).
DR HSSP; 077414; AAB80855.1; -.
DR HSSP; P00811; IC3B.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 381 AA; 41973 MW; BE366336B403A87F CRC64;

024684 Length: 381 March 17, 2003 12:32 Type: P Check: 557 ..
Found using 'KTXS' (swope073.key)

...

285 MYOGIGEMLMWPLKADSIINGSKVALALPAVEVNPAPAVKASVWHTGSGTGGFS
1--1
335
345 YVAFVPERNLGIWMLANKSYFNPVPRVPAWRILEKLO

-----
1 match found in sequence:
024823 ; SPT-1.
(from "lactxs_spt.pep")
TOIG of: 024823 check: 2776 from: 1 to: 378

ID 024823 PRELIMINARY; PRT; 378 AA.
AC 024823:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE SPT-1.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GN1694;
RX MEDLINE-98109336; PubMed-9449282;
RA Matsumura N., Minami S., Mitsuhashi S.;
RT "Sequences of homologous beta-lactamases from clinical isolates of
RT Serratia marcescens with different substrate specificities.";
RL Antimicrob. Agents Chemother. 42:176-179(1998).
DR HSSP; P05364; 2BLF.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 378 AA; 41357 MW; E5191588C858BACB CRC64;

024824 Length: 378 March 17, 2003 12:32 Type: P Check: 2639 ..
Found using 'KTXS' (swope073.key)

...

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RL Antimicrob. Agents Chemother. 42:176-179(1998).
DR EMBL; AB008454; BAA23130.1; -.
DR HSSP; P05364; 2BLF.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 378 AA; 41256 MW; BD425346BB146084 CRC64;

024823 Length: 378 March 17, 2003 12:32 Type: P Check: 2776 ..
Found using 'KTXS' (swope073.key)

...

280 FTODLMKMENTPYVKLSRLIEGNNAGIMNGTPPATAITPPPELRAKGYTKTGSGTGFST
1--1
330
340 YAVFIPAKNIYAVVMLANKWFPNDREVAAYHIVQALDKR

-----
1 match found in sequence:
026155 ; Conserved protein.
(from "lactxs_spt.pep")
TOIG of: 026155 check: 2682 from: 1 to: 450

ID 026155 PRELIMINARY; PRT; 450 AA.
AC 026155:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

...

```

DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE Conserved protein.
 GN MTH49.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
 RA Aldehyde T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pochier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 DR EMBL, AE000797; AAB84556.1; --
 DR InterPro: IPR001279; Bactlase-like.
 DR InterPro: IPR004613; MG423.
 DR InterPro: IPR001587; UPE0036.
 DR Pfam: PF00753; lactamase_B. 1.
 DR Pfam: PF02147; UPE0036; 1.
 DR TIGRfam: TIGR00649; MG423; 1.
 KW Complete proteome.
 SQ SEQUENCE 450 AA; 49983 MW; E35CA214F5A476B7 CRC64;

026155 Length: 450 March 17, 2003 12:32 Type: P Check: 2682 ..
 Found using 'KTXS' (swope073.key)

166 GIIVALDFKPPDHOKISPPDYHRLRLGRGVLAIVETTRANEKEVTHSKVARI
 216
 226 VLEDIMKNPLEEKGIMVTFTSSHMERIQAIISDIASKSDROML
 1 match found in sequence:
 o32352 ; Beta lactamase class C (Fragment).
 (from "lactxs_spt.pep")
 TOIG of: o32352 check: 748 from: 1 to: 381
 ID 032352 PRELIMINARY; PRT; 381 AA.
 AC 032352;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Beta lactamase class C (Fragment).
 GN BLA CF H224.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H224;
 RX MEDLINE=99085658; PubMed=9868767;
 RA Verdet C., Arlet G., Ben Redjeb S., Ben Hassan A., Lagrange P.H.,
 RA Philippou A.;
 RT "Characterization of CW-4, an AmpC-type plasmid-mediated beta-
 RT lactamase in a Tunisian clinical isolate of Proteus mirabilis.";
 RL FEMS Microbiol. Lett. 169:235-240(1998).
 DR EMBL, Y15129; CAAT5401.1; --
 DR HSSP, P00811; IC3B.
 DR InterPro: IPR001466; Beta_lactamase.

DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 FT NON_TER 381
 SQ SEQUENCE 381 AA; 42013 MW; 7EFD9C3A217D238 CRC64;
 032352 Length: 381 March 17, 2003 12:32 Type: P Check: 748 ..
 Found using 'KTXS' (swope073.key)

285 MYOGLGEMLNWPLKADSIINGSDSKVLAALPAVEVNPVPAVKASWVKTGSGGFGS
 335

345 YVAFVPEKNIGIYMLANKSYNPVRYEAMRILEKLO

1 match found in sequence:
 o32579 ; Beta-lactamase LAT-3 protein precursor.
 (from "lactxs_spt.pep")
 TOIG of: o32579 check: 9839 from: 1 to: 381

ID 032579 PRELIMINARY; PRT; 381 AA.
 AC 032579;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Beta-lactamase LAT-3 protein precursor.
 GN BLA LAT-3.
 OS Escherichia coli.
 OC Plasmid pMEL1.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99034048; PubMed=9818739;
 RA Gazouli M., Tzouveleakis L.S., Vatsopoulos A.C., Tzelepi E.;
 RT "Transferable class C beta-lactamases in Escherichia coli strains
 RT isolated in Greek hospitals and characterization of two enzyme
 RT variants (LAT-3 and LAT-4) closely related to Citrobacter freundii
 RT AmpC beta-lactamase.";
 RT J. Antimicrob. Chemother. 42:419-425(1998).
 DR EMBL, Y15411; CAAT5610.1; --
 DR HSSP, P00811; IC3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Plasmid; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 381 BETA-LACTAMASE LAT-3 PROTEIN.
 SQ SEQUENCE 381 AA; 41966 MW; F2005C8D0DBB2C0 CRC64;
 032579 Length: 381 March 17, 2003 12:32 Type: P Check: 9839 ..
 Found using 'KTXS' (swope073.key)

285 MYOGLGEMLNWPLKADSIINGSDSKVLAALPAVEVNPVPAVKASWVKTGSGGFGS
 335

345 YVAFVPEKNIGIYMLANKSYNPVRYEAMRILEKLO

1 match found in sequence:
 o32580 ; Beta-lactamase LAT-4 protein precursor.
 (from "lactxs_spt.pep")
 TOIG of: o32580 check: 9796 from: 1 to: 381

ID 032580 PRELIMINARY; PRT; 381 AA.

AC 032580;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta-lactamase LAT-4 protein precursor.
 GN BLA LAT-4.
 OS Escherichia coli.
 OC Plasmid pHEL2.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99034048; PubMed=9818739;
 RA Gazouli M., Tzouveleki L.S., Vatsopoulos A.C., Tzilepi E.;
 RT "Transferable class C beta-lactamases in Escherichia coli strains
 isolated in Greek hospitals and characterization of two enzyme
 variants (LAT-3 and LAT-4) closely related to Citrobacter freundii
 AmpC beta-lactamase.";
 RT J. Antimicrob. Chemother. 42:419-425(1998).
 RL EMBL: Y15412; CAA75611.1; -;
 DR HSSP: P00811; IC3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase.C.
 DR Pfam: PF00144; beta-lactamase_1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Plasmid; signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 381 BETA-LACTAMASE LAT-4 PROTEIN.
 SQ SEQUENCE 381 AA; 42021 MW; 8E46D8F2849703B CRC64;
 032580 Length: 381 March 17, 2003 12:32 Type: P Check: 9796 ..
 Found using 'KTXS' (swope073.key)

285 MYOGLGEMLNWPLKADSIINGSDSKVALALPAVEVNPAPAPAKASWVKTSGGFGS
 335
 345 YVAFVPEKNIGIVMLANKSYPNPVRVEAMRIELKIQ
 1 match found in sequence:
 033446 ; Beta-lactamase class C (CEPHAMYCINASE) (Fragment).
 (from "lactxs_spt.pep")
 TOIG of: 033446 check: 59 from: 1 to: 381
 ID 033446 PRELIMINARY; PRT; 381 AA.
 AC 033446;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta-lactamase class C (CEPHAMYCINASE) (Fragment).
 GN BLA CMY-3 OR CMY-4 OR BLACMY-4.
 OS Proteus mirabilis, and
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Proteus
 OX NCBI_TaxID=584, 562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H223B;
 RA Verdet C., Arlet G., Ben Redjeb S., Lagrange P.H., Philippin A.;
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22317, AND LAR;
 RA Decre D., Raskine L., Blancard H., Sanson-Le Pors M.J., Petit J.C.,
 RU Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=79;
 RA Stapleton P.D., Shannon K.P., French G.L.;
 RT "Carbapenem resistance in Escherichia coli associated with plasmid-
 determined CMY-4 beta-lactamase production and loss of an outer
 membrane protein.";
 RT membrane protein.
 RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RA Zhao S., White D.G., McDermott P.F., Walker R.D.;
 RT "Identification and Expression of Cephamycinase blaCMY Genes in
 Escherichia coli and Salmonella Isolated from Food Animals and Ground
 Meats.";
 RT
 RT
 RL Antimicrob. Agents Chemother. 0:0-0(2001).
 DR EMBL: Y15130; CAA75402.1; -;
 DR EMBL: Y16783; CAA76380.1; -;
 DR EMBL: Y16782; CAA76379.1; -;
 DR EMBL: AJ007826; CAA07695.1; -;
 DR EMBL: AF420597; AAL16928.1; -;
 DR HSSP: P00811; IC3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase.C.
 DR Pfam: PF00144; beta-lactamase_1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 FT NON_TER 381 381
 SQ SEQUENCE 381 AA; 41973 MW; CE62C01822AFC416 CRC64;
 033446 Length: 381 March 17, 2003 12:32 Type: P Check: 59 ..
 Found using 'KTXS' (swope073.key)

285 MYOGLGEMLNWPLKADSIINGSDSKVALALPAVEVNPAPAPAKASWVKTSGGFGS
 335
 345 YVAFVPEKNIGIVMLANKSYPNPVRVEAMRIELKIQ
 1 match found in sequence:
 033900 ; Hypothetical 72.6 kDa protein.
 (from "lactxs_spt.pep")
 TOIG of: 033900 check: 9983 from: 1 to: 661
 ID 033900 PRELIMINARY; PRT; 661 AA.
 AC 033900;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical 72.6 kDa protein.
 OS Shewanella sp. SCRC-2738.
 CC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 CC Shewanella.
 OX NCBI_TaxID=53560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SCRC-2738;
 RX MEDLINE=97419510; PubMed=9274025;
 RA Takeyama H., Takeda D., Yazawa K., Yamada A., Matsunaga T.;
 RT "Expression of the eicosapentaenoic acid synthesis gene cluster from
 Shewanella sp. in a transgenic marine cyanobacterium, Synechococcus
 sp.";
 RT Microbiology 143:0-0(0).
 RL EMBL: U73935; AAB81119.1; -;
 DR InterPro: IPR001279; Blactamase-like.
 DR Pfam: PF00753; lactamase_B; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 661 AA; 72619 MW; 438E6A62817F895E CRC64;
 033900 Length: 661 March 17, 2003 12:32 Type: P Check: 9983 ..
 Found using 'KTXS' (swope073.key)

483 VMAEPENDSARQLADTYEQLGQAEGAGWRNITLTGAQELKVGIOGAPFTASDVISE 1--1
533

543 MDMPLEFLAVKIDSQAQKHGLVKMNYITPDTKDIYIELSN

1 match found in sequence:
034177 ; Beta-lactamase CTX-M-3 (EC 3.5.2.6) (Beta-lactamase CTX-M-5).
(from "lactxs_spt.pep")
TOIG of: 034177 check: 8912 from: 1 to: 291

ID 034177 PRELIMINARY; PRT; 291 AA.
AC 034177;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Beta-lactamase CTX-M-3 (EC 3.5.2.6) (Beta-lactamase CTX-M-5).
GN BLACTX-M-3 OR KUDA-2 OR BLACTX-M-5.
OS Salmonella typhimurium, and
OC Kluysera ascorbata.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602, 51288;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-S. typhimurium;
RA Bradford P.A., Yang Y., Salm D.F., Grope I., Gardovska D., Storch G.;
RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-K. ascorbata; STRAIN=IP15.79;
RA Humenik C., Arlet G., Labia R., Philippou A.;
RL "Beta-lactamase of Kluysera ascorbata: progenitor of some plasmid-
RT encoded CTX-M types.";
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-S. typhimurium;
RA Humenik C., Arlet G., Labia R., Philippou A.;
RL "Beta-lactamase of Kluysera ascorbata: progenitor of some plasmid-
RT encoded CTX-M types.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)O = A SUBSTITUTED BETA-
AMINO ACID.
CC -1- SIMILARITY: THIS IS A CLASS-A BETA-LACTAMASE.
DR EMBL: U95364; AAC32890.1; -;
DR EMBL: AJ251722; CAB63259.1; -;
DR EMBL: AF286192; AAG24824.1; -;
DR HSSP: Q47066; 1BZA.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta_lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Antibiotic resistance; Hydrolase; Plasmid.
SQ SEQUENCE 291 AA; 31293 MW; 822C6D78D358BDB0 CRC64;
034177 Length: 291 March 17, 2003 12:32 Type: P Check: 8912 ..
Found using 'KTXS' (swope073.key)

187 LMAQTIKMLTGKALAFORQAQVLTWLGKNTTGSASIRAGLPKSGVGDGKTSQSDYGT 1--1
237

247 NDIATVWPNHAPLVLYTFTPEOKAESRRDYLAAAKIYTHG

1 match found in sequence:
044476 ; Hypothetical 93.9 kDa protein.
(from "lactxs_spt.pep")

TOIG of: 044476 check: 7390 from: 1 to: 833

ID 044476 PRELIMINARY; PRT; 833 AA.
AC 044476;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Hypothetical 93.9 kDa protein.
GN E04A4.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA MEDLINE=99069613; Pubmed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Sammons L., Wohlmann P., Biewald T.;
RT "The sequence of C. elegans cosmid E04A4.";
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submision.";
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF038611; AAB92042.3; -;
DR InterPro: IPR001279; Blactamase-like.
DR Pfam: PF00753; lactamase_B; 2.
KW Hypothetical protein.
SQ SEQUENCE 833 AA; 93864 MW; 3803C0A48C99F143 CRC64;

044476 Length: 833 March 17, 2003 12:32 Type: P Check: 7390 ..
Found using 'KTXS' (swope073.key)

551 LNCVLITHAQDHNGLYTIIRKKEAFESLGAPRYPLVLCNRNVLKPKKTSICPNT 1--1
601

611 EHLEIVDISRYPLTPPGSGPGPKRRPLSPHLPSPDVLAD

1 match found in sequence:
052904 ; ES-beta-lactamase (EC 3.5.2.6) (CTX-M-3 type beta-lactamase).
(from "lactxs_spt.pep")
TOIG of: 052904 check: 306 from: 1 to: 291

ID 052904 PRELIMINARY; PRT; 291 AA.
AC 052904;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE ES-beta-lactamase (EC 3.5.2.6) (CTX-M-3 type beta-lactamase).
GN BLA CTX-M-3 OR BLA CTX-M-3.
OS Citrobacter freundii, and
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

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OC Citrobacter.
OX NCBI_TaxID=546, 545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=C.freundii; STRAIN=CLIS1 2526/96;
RX MEDLINE=9817104; PubMed=9517925;
RA Gniadkowski M., Schneider I., Jungwirth R., Hryniewicz W.,
  Baurenfeind A.;
RT "cefotaxime-resistant Enterobacteriaceae isolates from three Polish
  hospitals: identification of three novel TEM- and SHV-5-type extended-
  spectrum beta-lactamases.";
RL Antimicrob. Agents Chemother. 42:514-520(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=C.freundii; STRAIN=CLIS1 2526/96;
RX MEDLINE=98218693; PubMed=9559791;
RA Gniadkowski M., Schneider I., Palucha A., Jungwirth R., Mikielwicz B.,
  Baurenfeind A.;
RT "cefotaxime-resistant Enterobacteriaceae isolates from a hospital in
  Warsaw, Poland: identification of a new CTX-M-3 cefotaxime-hydrolyzing
  beta-lactamase that is closely related to the CTX-M-1/MEN-1 enzyme.";
RL Antimicrob. Agents Chemother. 42:827-832(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=C.diversus; STRAIN=KHS13; PLASMID=PKCSM13;
RA Sekiguchi J., Morita K., Watanabe N., Wada H., Okazaki M.,
  Kanamori M.;
RT "Plasmid-mediated CTX-M-3 type beta lactamase isolated from
  Citrobacter koseri in Japan.";
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)O = A SUBSTITUTED BETA-
  AMINO ACID.
CC -1- SIMILARITY: THIS IS A CLASS-A BETA-LACTAMASE.
DR EMBL: Y10278; CAA71321.1; -.
DR EMBL: AB059404; BAB40925.1; -.
DR HSSP: Q47066; 1BZA.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta_lactamase; 1.
DR PRINTS: PR00118; BETA_LACTAMASE_A; 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Antibiotic resistance; Hydrolase; Plasmid.
SQ SEQUENCE 291 AA; 31201 MW; 49c77ACA61F07B4A CRC64;

052904 Length: 291 March 17, 2003 12:32 Type: P Check: 306
Found using 'KTXS' (swope073.key)

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187 RAMAQTLRRLTLGKALGDSQRAQLVTMMKMTTGAASIQAGLPSAWVVGDXGTGSGDYCTT
133
247 NDIAVIMPKDRAPLILVTYTFQPPKAEKSRDVLASAKIYTDG
237

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2 matches found in sequence:
052988 ; ES-beta-lactamase precursor.
(from "lactxs_spt.pep")
TOIG of: 052988 check: 7221 from: 1 to: 382

ID 052988 PRELIMINARY; PRT; 382 AA.
AC 052988;
DR 01-JUN-1998 (TREMBLrel. 06, Created)
DR 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DR 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ES-beta-lactamase precursor.
GN BLA-FOX-2.
OS Escherichia coli.
OG Plasmid pMVP-7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

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OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BM U2206;
RX MEDLINE=97447673; PubMed=9303413;
RA Baurenfeind A., Wagner S., Jungwirth R., Schneider J., Meyer D.;
RT "A novel class C beta-lactamase (FOX-2) in Escherichia coli
  conferring resistance to cephalosporins.";
RL Antimicrob. Agents Chemother. 41:2041-2046(1997).
DR EMBL: Y10282; CAA71325.1; -.
DR HSSP: P05364; 2B1T.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta_lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW Plasmid; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 382 POTENTIAL.
SQ SEQUENCE 382 AA; 40935 MW; 13E3B3804035B885 CRC64;

052988 Length: 382 March 17, 2003 12:32 Type: P Check: 7221
Found using 'KTXS' (swope073.key)

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196 SQTLLPKGLHHYIYQVESAMANYAYGSKEDKPIRVTPGVLAELVYKIGTSADLLK
133
236 VEANNGYOGDAALKAIALALHTGFGYSVGDWTOGLGMSVAYPYTEQALLAGNSPAVSFOA
246
316 NPVTRFAPVPMKMGQRILNKTGSGRGAVVAPFAPGALIVMLANRPTEARVKAHA
335
376 ILSQLAE
133

-----
1 match found in sequence:
053044 ; Beta-lactamase class C (Fragment).
(from "lactxs_spt.pep")
TOIG of: 053044 check: 59 from: 1 to: 381

ID 053044 PRELIMINARY; PRT; 381 AA.
AC 053044;
DR 01-JUN-1998 (TREMBLrel. 06, Created)
DR 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DR 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-lactamase class C (Fragment).
GN BLA CMY-3.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
  Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCH 9701;
RA Decre D., Raskine L., Blanchard H., Sanson-Le Pors M.J., Petit J.C.,
  Philippon A., Arlet G.;
RT "Importation and characterization of CMY-type beta-lactamases from
  Proteus mirabilis and Klebsiella pneumoniae in four parisian
  hospitals.";
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: Y16781; CAA76378.1; -.
DR HSSP: P00811; 1C3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta_lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
FT NON_TER 381 381
SQ SEQUENCE 381 AA; 41973 MW; CB62C01822AFC416 CRC64;

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OS044 Length: 381 March 17, 2003 12:32 Type: P Check: 59 ..
Found using 'ktxs' (swope073.key)

285 MYGIGWEMLMWPLKADSIINGSDSKVALAALPAVEVNPAPAVAKSWVHTGSGTGGFGS
335

345 YVAFVPEKNLGIWMLANKSYNPVPEVPEAMRLEKIQ

1 match found in sequence:
054038 : Beta-lactamase class C (Fragment).
(from "lactxs_spt.pep")
TOIG of: 054038 check: 980 from: 1 to: 381

ID 054038 PRELIMINARY; PRT; 381 AA.
AC 054038;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-lactamase class C (Fragment).
GN BLA CM-4.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-34955;
RA Decre D., Raskine L., Blanchard H., Sanson-Le Pors M.J., Petit J.C.,
RA Philippon A., Arlet G.;
RT "Importation and characterization of CM- type beta-lactamases from
RT Proteus mirabilis and Klebsiella pneumoniae in four parisian
RT hospitals.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y16785; CA676382.1; -.
DR HSSP: P00811; 1C3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; Beta_lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
FT NON_TER 381
SQ SEQUENCE 381 AA; 42016 MM; 6323F9CECC7C3A1A CRC64;
OS0438 Length: 381 March 17, 2003 12:32 Type: P Check: 980 ..
Found using 'ktxs' (swope073.key)

285 MYGIGWEMLMWPLKADSIINGSDSKVALAALPAVEVNPAPAVAKSWVHTGSGTGGFGS
335

345 YVAFVPEKNLGIWMLANKSYNPVPEVPEAMRLEKIQ

1 match found in sequence:
055601 : Replisase.
(from "lactxs_spt.pep")
TOIG of: 055601 check: 5449 from: 1 to: 1550

ID 055601 PRELIMINARY; PRT; 1550 AA.
AC 055601;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Replisase.
OS Garlic virus C.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Allexivirus.
OX NCBI_TaxID=12431;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=93389442; PubMed=8376963;
RA Sumi S., Tsuneyoshi T., Furutani H.;
RT "Novel rod-shaped viruses isolated from garlic, Allium sativum,
RT possessing a unique genome organization.";
RL J. Gen. Virol. 74:1879-1885(1993).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=20009173; PubMed=10542028;
RA Sumi S., Matsumi T., Tsuneyoshi T.;
RT "Complete nucleotide sequences of garlic viruses A and C, members of
RT the newly ratified genus Allexivirus.";
RL Arch. Virol. 144:1819-1826(1999).
DR EMBL: AB010302; BAA61818.1; -.
DR InterPro: IPR000871; Beta_lactamase_A.
DR InterPro: IPR001788; RNA_dep_RNAPol2.
DR InterPro: IPR000606; Viral_helicase1.
DR Pfam: PF00978; RNA_dep_RNAPol2; 1.
DR Pfam: PF01443; Viral_helicase1; 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 1550 AA; 174874 MM; 0C0A75334938F4E7 CRC64;
OS05601 Length: 1550 March 17, 2003 12:32 Type: P Check: 5449 ..
Found using 'ktxs' (swope073.key)

450 NLNGAGOREGERGEHAHGNQNTSTPPPHQSPHDAAGSSSEAKRTSSDEPEV
500

510 SKCDEEDLGSCTSDGHTWDSSESDSCDDKHQIFDSLSPFT

1 match found in sequence:
055647 : G2-G1 polypotein.
(from "lactxs_spt.pep")
TOIG of: 055647 check: 5304 from: 1 to: 1135

ID 055647 PRELIMINARY; PRT; 1135 AA.
AC 055647;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE G2-G1 polypotein.
OS tomato spotted wilt virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tosopovirus.
OX NCBI_TaxID=11613;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsuda S.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ohnishi J., Kirita M., Hosokawa D., Tsuda S.;
RT "Sequence analysis for M RNA segment of tomato spotted wilt tospovirus
RT isolated in Japan.";
RL Ann. Phytopathol. Soc. Jpn. 63:277-277(1997).
DR EMBL: AB010996; BAA24894.1; -.
DR InterPro: IPR000871; Beta_lactamase_A.
DR InterPro: IPR005167; Bunya_G1.
DR Pfam: PF03557; Bunya_G1; 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Polypotein.
SQ SEQUENCE 1135 AA; 127332 MM; BD9977103BE957F2 CRC64;

OS05647 Length: 1135 March 17, 2003 12:32 Type: P Check: 5304 ..
Found using 'ktxs' (swope073.key)

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53      ENVEPTASIORKALLETFTNLMEESQTPGTRQIREGESIIPRFAESNTOKTTSVDLPN
      |--|
      103

113      NCLNASSLKEIKGVSTYNYVYGVNNGVYSCVSDSAEGLK
      |--|
      103

1 match found in sequence:
058798 ; Hypothetical protein PH1071.
(from "lactxs_spt.pep")
TOIG of: 058798 check: 489 from: 1 to: 450

ID 058798      PRELIMINARY;      PRT;      450 AA.
AC 058798;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein PH1071.
GN PH1071.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguni A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL: AP000004; BAA30170.1; -
DR InterPro: IPR001279; Blactamase-like.
DR InterPro: IPR004613; MG423.
DR InterPro: IPR001587; UPF0036.
DR Pfam: PF00753; lactamase_B; 1.
DR Pfam: PF02147; UPF0036; 1.
DR TIGRfams: TIGR00649; MG423; 1.
DR PROSITE: PS01292; UPF0036; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 450 AA; 50341 MW; 4f8833725b966dfb CRC64;

058798 Length: 450 March 17, 2003 12:32 Type: P Check: 489 ..
Found using 'KTXS' (swope073.key)

...

172      PEGAVVAYADYKFDNNHPYGEKPKYRKLKELGKGVVLIAESTRAVEETKTSSEAVAKM
      |--|
      222

232      LLEDFLEGMADGLATTFASHIARLQELIETANKMGROAIR
      |--|
      222

1 match found in sequence:
066831 ; Penicillin binding protein 2.
(from "lactxs_spt.pep")
TOIG of: 066831 check: 1457 from: 1 to: 578

ID 066831      PRELIMINARY;      PRT;      578 AA.
AC 066831;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

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DE Penicillin binding protein 2.
GN PBP2 OR AQ.556.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL: AE000695; AAC06783.1; -
DR InterPro: IPR000871; Beta_lactamase_A.
DR InterPro: IPR005311; PBP_dimer.
DR InterPro: IPR001460; Transpeptidase.
DR Pfam: PF03717; PBP_dimer; 1.
DR Pfam: PF00905; Transpeptidase; 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Complete proteome.
SQ SEQUENCE 578 AA; 67202 MW; 9BBFC3F7240BC59 CRC64;

066831 Length: 578 March 17, 2003 12:32 Type: P Check: 1457 ..
Found using 'KTXS' (swope073.key)

...

465      EKIQIKSTVKNIRDLVIEVEKGTGKRAKSEYFAGKGTGAQKYDSALKTYSREKLVT
      |--|
      515

525      YELGFPESEPKFTVLILVDEPKKNLYGCTVAAPYFKELIEKIG
      |--|
      515

1 match found in sequence:
069409 ; AmpC-type beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: 069409 check: 744 from: 1 to: 381

ID 069409      PRELIMINARY;      PRT;      381 AA.
AC 069409;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE AmpC-type beta-lactamase.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=550;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98377722; PubMed=9711843;
RA Morosini M.I., Negri M.C., Sholchet B., Baquero M.R., Baquero F.,
RA Blazquez J.;
RT "An extended-spectrum AmpC-type beta-lactamase obtained by in vitro
RT antibiotic selection.";
RL FEMS Microbiol. Lett. 165:85-90(1998).
DR EMBL: AJ005633; CA06639.1; -
DR HSP: P05364; 2BLT.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 41301 MW; 49D127F268B75C3C CRC64;

069409 Length: 381 March 17, 2003 12:32 Type: P Check: 744 ..
Found using 'KTXS' (swope073.key)

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285 MYOGLGEMLMNPVANTVVEGSDSKVALALPLPAEAVNPAPAPYKASWHTGSGTSGRGS
335

345 YVAFIPEKELGIVMLANKSYNPAPARVEAAVHILEALQ

1 match found in sequence:
081069 ; Putative receptor-like protein kinase.
(from "lactxs_spt.pep")
TOIG of: 081069 check: 7605 from: 1 to: 884

ID 081069 PRELIMINARY; PRT; 884 AA.
AC 081069;
DT 01-NOV-1998 (TRMBLrel. 08, Created)
DT 01-NOV-1998 (TRMBLrel. 08, last sequence update)
DT 01-MAR-2002 (TRMBLrel. 20, Last annotation update)
DE Putative receptor-like protein kinase.
GN AT2G28990.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanden S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Salzberg S.L., Fraser C.M., Venter W.C., White O., Eisen J.A.,
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana";
RT Nature 402:761-768(1999).
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RU Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AC005315; AAC33227.1; -.
DR InterPro: IPR000871; Beta_lactamase_A.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR Pfam: PF00560; LRR; 3.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00370; LRR; 2.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferrase.
SQ SEQUENCE 884 AA; 98755 MW; E354E899PAAE48BE CRC64;

081069 Length: 884 March 17, 2003 12:32 Type: P Check: 7605 ..
Found using 'ktxs' (swope073.key)

403 TSPFIISDLKSGKNGSIPIQLNFTQLDELDSNNSLTGPPVIFLANKTSLINLMSG

463 NNLGSGVPQALLDKEKGLVLEGNPDLCSSFCNTEKKNKFL

2 matches found in sequence:
083024 ; Ampc protein.
(from "lactxs_spt.pep")
TOIG of: 083024 check: 570 from: 1 to: 381

ID 083024 PRELIMINARY; PRT; 381 AA.
AC 083024;
DT 01-NOV-1998 (TRMBLrel. 08, Created)
DT 01-NOV-1998 (TRMBLrel. 08, last sequence update)
DT 01-JUN-2002 (TRMBLrel. 21, Last annotation update)
DE Ampc protein.
GN AMPC.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GN7471;
RX MEDLINE=20145369; PubMed=10681318;
RA Kuga A., Okamoto R., Inoue M.;
RT "amp^r gene mutations that greatly increase class C beta-lactamase
activity in enterobacter cloacae";
RL Antimicrob. Agents Chemother. 44:561-567(2000).
DR EMBL: AB016611; BAA32077.1; -.
DR HSSP: P05364; 2BLT.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 41458 MW; D2EB2572692C4210 CRC64;

083024 Length: 381 March 17, 2003 12:32 Type: P Check: 570 ..
Found using 'ktxs' (swope073.key)

1 MKTRSLCALLLSTSCSVLAAPMSEKQLSDVVERTYPLMKAAIIPGMVAVIYQ
2 5

285 MYOGLGEMLMNPVEAKTYVEGSDNKVALALPLPAEAVNPAPAPYKASWHTGSGTSGRGS
335

345 YVAFIPEKELGIVMLANKSYNPAPARVEAAVHILEALQ

1 match found in sequence:
087489 ; Beta-lactamase CEF-1 precursor (EXTENDED SPECTRUM beta lactamase)
(from "lactxs_spt.pep")
TOIG of: 087489 check: 6246 from: 1 to: 299

ID 087489 PRELIMINARY; PRT; 299 AA.
AC 087489;
DT 01-NOV-1998 (TRMBLrel. 08, Created)
DT 01-NOV-1998 (TRMBLrel. 08, last sequence update)
DT 01-MAR-2002 (TRMBLrel. 20, Last annotation update)
DE Beta-lactamase CEF-1 precursor (EXTENDED SPECTRUM beta lactamase)
DE (EXTENDED-SPECTRUM beta-lactamase VEB-1).
GN BLACEF-1 OR VEB-1 OR BLAEB-1.
OS Pseudomonas aeruginosa,
OS Pseudomonas mirabilis,
OS Escherichia coli, and
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.

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OX NCBI_TaxID=287, 562, 584;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.aeruginosa; STRAIN=PAH2;
RA Tripathi C., Fennwald M.A.;
RT "Ceftazidime and rifampin resistance gene cassettes in an integron
  from Pseudomonas aeruginosa."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli, and P.aeruginosa; STRAIN=MG-1;
RA Naas T., Poirol L., Guibert M., Labia R., Nordmann P.;
RT "Molecular characterization of VEB-1, a novel Extended-Spectrum Beta-
  lactamase from Escherichia coli."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=P.aeruginosa; STRAIN=JES;
RX MEDLINE=99169778; PubMed=10049290;
RA Poirol L., Naas T., Guibert M., Chaibi E., Labia R., Nordmann P.;
RT "Many class I integrons comprise distinct stable structures occurring
  in different species of Enterobacteriaceae isolated from widespread
  geographic regions in Europe."
RL Antimicrob. Agents Chemother. 43:686-689(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli, and P.mirabilis; TRANSPOSON=TN2000;
RX MEDLINE=99169757;
RA Poirol L., Naas T., Guibert M., Chaibi E.B., Labia R., Nordmann P.;
RT "Molecular and biochemical characterization of VEB-1, a novel class A
  extended-spectrum beta-lactamase encoded by an Escherichia coli
  integron gene."
RL Antimicrob. Agents Chemother. 43:573-581(1999).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; TRANSPOSON=TN2000;
RX MEDLINE=2056689; PubMed=11114922;
RA Naas T., Mikami Y., Imai T., Poirol L., Nordmann P.;
RT "Characterization of In53, a class I plasmid- and composite
  transposon-located integron of Escherichia coli which carries an
  unusual array of gene cassettes."
RL J. Bacteriol. 183:235-249(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=P.mirabilis;
RA Naas T., Benoudia F., Massuard S., Nordmann P.;
RT "Integron-located VEB-1 extended-spectrum beta-lactamase gene in a
  Proteus mirabilis clinical isolate."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078527; AAC64364.1; -
DR EMBL; AF010416; AAD01435.1; -
DR EMBL; AF133699; AAD39933.1; -
DR EMBL; AF205943; AAG45716.1; -
DR EMBL; AF220758; AAK00603.1; -
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 299 AA; 33735 MW; BA9A70D85784C37F CRC64;
087489 Length: 299 March 17, 2003 12:32 Type: P Check: 6246
Found using 'KTXS' (swope073.key)

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2 matches found in sequence:
087643 ; Beta-lactamase.
(from "ktxs_spt.pep")
TOIG of: 087643 check: 6263 from: 1 to: 295
ID 087643 PRELIMINARY; PRT; 295 AA.
AC 087643;
DT 01-NOV-1998 (TRENBLREL. 08, Created)
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
DE 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Beta-lactamase.
GN BLA.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99318622; PubMed=10390247;
RA Weng S.F., Chen C.Y., Lee Y.S., Lin J.W., Tseng Y.H.;
RT "Identification of a novel beta-lactamase produced by Xanthomonas
  campestris, a phytopathogenic bacterium."
RL Antimicrob. Agents Chemother. 43:1792-1797(1999).
DR EMBL; AF091319; AAC43036.1; -
DR HSP: P00810; ITEM.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; B_LACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 295 AA; 31806 MW; 868E71485F3422AA CRC64;
087643 Length: 295 March 17, 2003 12:32 Type: P Check: 6263
Found using 'KTXS' (swope073.key)
-----
115 TERNHVGSGSLVAELCOATMTHSDNPANLFLPLIGDPPELTFRFLGIGDTKRSRLKAM
165
175 NGFAPEPRDTTTPAAMATLRLTLGLDALQPASRKQLTAMWIDNRFGDDCLRAGLPRDW
235 KIDKRGSGTGTDRNDIAIIPPGRAAPLLIAYLNGATVDAARDALKVAEAVRD
239
-----
2 matches found in sequence:
p71420 ; ES-beta-lactamase precursor.
(from "ktxs_spt.pep")
TOIG of: p71420 check: 9855 from: 1 to: 382
ID p71420 PRELIMINARY; PRT; 382 AA.
AC p71420;
DT 01-FEB-1997 (TRENBLREL. 02, Created)
DT 01-FEB-1997 (TRENBLREL. 02, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE ES-beta-lactamase precursor.
GN BLA(CMY-1).
OS Klebsiella pneumoniae.
OG Plasmid pMVP-1.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHO;

```

RX MEDLINE=9700164; PubMed=843306;
 RA Baerenteind A., Stemplinger I., Chong Y.;
 RT "Comparative characterization of the cephamycinase blaCMY-1 gene and
 its relationship to other beta-lactamase genes";
 RL Antimicrob. Agents Chemother. 40:1926-1930(1996).
 DR EMBL; X92508; CAA63264.1; -.
 DR HSSP; P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam; PF00144; beta-lactamase; 1.
 DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
 KW Plasmid; Signal.
 FT SIGNAL 1 23 POTENTIAL.
 SQ SEQUENCE 382 AA; 40825 MW; 7E003A4B20D594DB CRC64;
 P71420 Length: 382 March 17, 2003 12:32 Type: P Check: 9855 ..
 Found using 'KTXS' (swope073.key)

199 E0TLPLGLMHTYVNPQKQAMASYAGSKEDKPIRVNPGMLADEAYGKTSADILRF
 249
 259 VKANIGGVDDKALQQAISLTHQGHVSGWMTQGLGWESYAVPYTEQTLNLSAKVILEA
 319 NPTAPRESQVLEPNKGTSTNGFGAYVAVPARGIIVMLANNPNPNAIRAKAAHAILA
 335
 379 QLAG

 2 matches found in sequence:
 p94288; Alkaline D-peptidase.
 (from "lactxs_spt.pep")
 TOIG of: p94288 check: 9557 from: 1 to: 388
 ID P94288 PRELIMINARY; PRT; 388 AA.
 AC P94288;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Alkaline D-peptidase.
 GN ADP.
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SOIL, AND DF4-B;
 RX MEDLINE=97094745; PubMed=8939979;
 RA Asano Y., Ito H., Dairi T., Kato Y.;
 RT "An alkaline D-sterespecific endopeptidase with beta-lactamase
 activity from Bacillus cereus";
 RL J. Biol. Chem. 271:30256-30262(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DF4-B;
 RA Komeda H., Fukasawa M., Asano Y.;
 RT "Occurrence of alkaline D-peptidase homolog in Bacillus cereus DF4-
 B";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D86380; BAA13079.1; -.
 DR EMBL; AB041948; BAB69971.1; -.
 DR HSSP; P15555; 3PTE.
 DR MEROPS; S12.003; -.
 SQ SEQUENCE 388 AA; 42035 MW; 78F5779AF6A45556 CRC64;
 P94288 Length: 388 March 17, 2003 12:32 Type: P Check: 9557 ..
 Found using 'KTXS' (swope073.key)

1 1
 2 5
 61 L0LGFPEGLIAKTSSEGGKTSWYAGVANSKSKPMKTDFFRIGSVTKTFTATVQLAAE
 77 80
 121 NRIILDDSTIE

 2 matches found in sequence:
 p94856; Beta-lactamase class C.
 (from "lactxs_spt.pep")
 TOIG of: p94856 check: 9952 from: 1 to: 382
 ID P94856 PRELIMINARY; PRT; 382 AA.
 AC P94856;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta-lactamase class C.
 GN BLA FOX-3.
 OS Klebsiella oxytoca.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=571;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1731;
 RX MEDLINE=98139051; PubMed=9527810;
 RA Marchese A., Arlet G., Schito G.C., Lagrange P.H., Philippon A.;
 RT "Characterization of FOX-3, an AmpC-type plasmid-mediated beta-
 lactamase from Italian Klebsiella oxytoca and Klebsiella pneumoniae
 isolates";
 RL Antimicrob. Agents Chemother. 42:464-467(1998).
 DR EMBL; Y11068; CAA71947.1; -.
 DR HSSP; P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam; PF00144; beta-lactamase; 1.
 DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 382 AA; 40993 MW; E38BD6C22C2F41EF CRC64;
 P94856 Length: 382 March 17, 2003 12:32 Type: P Check: 9952 ..
 Found using 'KTXS' (swope073.key)

196 S0TLPLGLMHTYVNPESAMANNVAGYSKEDKPIRVTPGVLAEAAYIKGSADLKE
 246
 256 AEAANMGVGGDALVKSAIALTHGTGYSVGEWTOGLGWESYDYPYTEQVLLAGNSPAVSFOA
 316 NPVTRFAPVPRAMGEORLYNKGSTGGFGAYVAVPARGIATVMLANNPNPPIARVAKAHA
 335
 376 ILSQLAE

 2 matches found in sequence:
 q44219; Cephalosporinase.
 (from "lactxs_spt.pep")
 TOIG of: q44219 check: 451 from: 1 to: 382
 ID Q44219 PRELIMINARY; PRT; 382 AA.
 AC Q44219;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Cephalosporinase.
OS Aeromonas sobria.
OC Bacteria: Proteobacteria; gamma subdivision; Aeromonadaceae;
OC Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AER 14;
RX MEDLINE=95110071; PubMed=7811022;
RA Rasmussen B.A., Keeney D., Yang Y., Bush K.;
RT "Cloning and expression of a cloxacillin-hydrolyzing enzyme and a
RT cephalosporinase from Aeromonas sobria AER 14M in Escherichia coli:
RT requirement for an E. coli chromosomal mutation for efficient
RT expression of the class D enzyme.";
RL Antimicrob. Agents Chemother. 38:2078-2085(1994).
DR EMBL: U10250; AAA83416.1; -.
DR HSSP: P05364; 2BLT.
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW Porin.
SQ SEQUENCE 382 AA; 40742 MW; 05128B06FEE6B5 CRC64;
Q44219 Length: 382 March 17, 2003 12:32 Type: P Check: 451 ..
Found using 'KTXS' (swope073.key)
...
196 SQTLLPGIALLPPTSRCLRGMDYAYCAKEKPIRVNPGVLADAYGIGIKTSADLLAF 1--1
246
256 VKANISGVDDKALQQAIALTHGTGFRIGEMSGIGMESYAVPVSEQTLLAGNSAVIYNA
316 NPKVPVAAQSEGTGARLNKSTGNGGAYVAFVPAKGIGIYMLANRNPVNDARVAAAYA 1--1
335
376 ILSKLAD
-----
2 matches found in sequence:
q44260 ; Ceps beta-lactamase.
(from "lactkxs_spl.pep")
TOIG of: q44260 check: 6423 from: 1 to: 382
ID Q44260 PRELIMINARY; PRT; 382 AA.
AC Q44260;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Ceps beta-lactamase.
GN CEPS.
OS Aeromonas sobria.
OC Bacteria: Proteobacteria; gamma subdivision; Aeromonadaceae;
OC Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96051676; PubMed=8537283;
RA Walsh T., Hall L., Macgowan A.P., Bennett P.M.;
RT "Sequence analysis of two chromosomally mediated inducible B-
RT lactamases from Aeromonas sobria, strain 163a, one a class D
RT penicillinase, the other an AmpC cephalosporinase.";
RL J. Antimicrob. Chemother. 36:41-52(1995).
DR EMBL: X80277; CAA56561.1; -.
DR HSSP: P05364; 2BLT.
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.

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SQ SEQUENCE 382 AA; 40613 MW; 6574DC48B47E82C5 CRC64;
Q44260 Length: 382 March 17, 2003 12:32 Type: P Check: 6423 ..
Found using 'KTXS' (swope073.key)
...
196 EQTLPLALGLEHTYIQVPEAAMARAFYKSKEDKPIRVNPGMLADEAYGIGIKTSADLLAF 1--1
246
256 VKANISGVDDKALQQAIALTHGTGFRIGEMSGIGMESYAVPVSEQTLLAGNSAVLSKA
316 NPVTKEFPAPAGMARLNKSTGSGFGAYVAFVPAKGIGIYMLANRNPVIEARVSAHA 1--1
335
376 ILSQLAP
-----
1 match found in sequence:
q45414 ; 'lipo-penicillinase' precursor.
(from "lactkxs_spl.pep")
TOIG of: q45414 check: 6233 from: 1 to: 310
ID Q45414 PRELIMINARY; PRT; 310 AA.
AC Q45414;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, last annotation update)
DE 'lipo-penicillinase' precursor.
OS Bacillus sp.
OC Bacteria: Firmicutes: Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=170;
RA Kato C.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=170;
RX MEDLINE=89245965; PubMed=2655551;
RA Kato C., Nakano Y., Horikoshi K.;
RT "The nucleotide sequence of the lipo-penicillinase gene of an
RT alkalophilic Bacillus sp. strain 170.";
RL Arch. Microbiol. 151:91-94(1989).
DR EMBL: D10848; BAA01621.1; -.
DR HSSP: P00808; 4BLM.
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Signal.
FT SIGNAL 1 29 POTENTIAL.
SQ SEQUENCE 310 AA; 34499 MW; 882019D569BE49A CRC64;
Q45414 Length: 310 March 17, 2003 12:32 Type: P Check: 6233 ..
Found using 'KTXS' (swope073.key)
...
201 KALATSLQAVALGDIIVSENRNFLIDMKRTTGTGDNILRAGVPGEMVPPKGTSGSYGTR 1--1
251
261 NDIAFIWPPNKKPFLIALISNQAKEDAKYDDKLIADATKIVLDV
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1 match found in sequence:
 q46038 ; Beta-lactamase.
 (from "lactxs_spt.pep")
 TOIG of: q46038 check: 450 from: 1 to: 381

ID Q46038 PRELIMINARY; PRT; 381 AA.
 AC Q46038;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-lactamase.
 GN AMP.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1113;
 RA Bennet P.M., Damdinsuren E., Jones M.E.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X76636; CA54084.1; -.
 DR HSSP: P00811; IC3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 381 AA; 42109 MW; E7DE776FF2419B34 CRC64;

Q46038 Length: 381 March 17, 2003 12:32 Type: P Check: 450 ..
 Found using 'KTXS' (swope073.key)

285 MYGIGWEMLMNPVKADIVINGSKIALALPAVEVNPAPVAVKASWVHTGSGFGS
 335

345 YVAFPEKNLGIIVMLANKSYNPAPVAVDAWRIELEKQ

1 match found in sequence:
 q46041 ; Beta-lactamase.
 (from "lactxs_spt.pep")
 TOIG of: q46041 check: 1146 from: 1 to: 381

ID Q46041 PRELIMINARY; PRT; 381 AA.
 AC Q46041;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta-lactamase.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GC3;
 RA Haruta S., Taniguchi K., Nakaya M., Sawai T.;
 RL "The nucleotide sequence and characterization of the extended-spectrum
 RT class C beta-lactamase from Citrobacter freundii GC3."
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D85910; BA12916.1; -.
 DR HSSP: P00811; IC3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 381 AA; 41841 MW; 5D70308A5C7FD370 CRC64;

Q46041 Length: 381 March 17, 2003 12:32 Type: P Check: 1146 ..
 Found using 'KTXS' (swope073.key)

285 MYGIGWEMLMNPVKADSIINGSDSKVALALPAVEVNPAPVAVKASWVHTGSGFGS
 335

345 YVAFPEKNLGIIVMLANKSYNPAPVAVDAWRIELEKQ

1 match found in sequence:
 q46991 ; Imi-1.
 (from "lactxs_spt.pep")
 TOIG of: q46991 check: 726 from: 1 to: 292

ID Q46991 PRELIMINARY; PRT; 292 AA.
 AC Q46991;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Imi-1.
 GN IMTA.
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1413B;
 RX MEDLINE=97032837; Pubmed=8878585;
 RA Rasmussen B.A., Bush K., Keeney D., Yang Y., Hare R., O'Gara C.,
 RA Medeiros A.A.;
 RT "Characterization of IMI-1 beta-lactamase, a class A carbapenem-
 RT hydrolyzing enzyme from Enterobacter cloacae."
 RL Antimicrob. Agents Chemother. 40:2080-2086 (1996).
 DR EMBL: U50278; AAA93461.1; -.
 DR HSSP: P52663; 1BUU.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 SQ SEQUENCE 292 AA; 32020 MW; A50A4C5DF1645615 CRC64;

Q46991 Length: 292 March 17, 2003 12:32 Type: P Check: 726 ..
 Found using 'KTXS' (swope073.key)

186 AAVAKSLKTLALGNILNERKETVQTWLKGNTTGAAIRIRASVPDWMYVGDKTCGCAYGT
 236

246 ANDYAVVWPKNRAPLIISVYTRNEKEAKHEDKVIAEASRIAD

1 match found in sequence:
 q48428 ; Beta-lactamase ACT-1.
 (from "lactxs_spt.pep")
 TOIG of: q48428 check: 4454 from: 1 to: 381

ID Q48428 PRELIMINARY; PRT; 381 AA.
 AC Q48428;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta-lactamase ACT-1.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-MCQ-95;
 RX MEDLINE=97209051; PubMed=9055993;
 RA Bradford P.A., Urban C., Mariano N., Projan S.J., Rahal J.J., Bush K.;
 RT "Innate resistance in *Klebsiella pneumoniae* is associated with the
 RT combination of ACT-1, a plasmid-mediated AmpC beta-lactamase, and the
 RT loss of an outer membrane protein."
 RL Antimicrob. Agents Chemother. 41:563-569(1997).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-MCQ-95;
 RA Bradford P.A., Urban C., Mariano N., Rahal J.J., Bush K.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U58495; AAC45086.2; -;
 DR HSSP: P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; Beta_lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 381 AA; 41572 MW; 3A5038DDA7DE3878 CRC64;

Q48428 Length: 381 March 17, 2003 12:32 Type: P Check: 4454
 Found using 'KTXS' (swope073.key)

286 MYGIGMEMLNMPYDAKTVEGSDNKVALAPLPAVEVNPAPVAVKSWHKSTGSGFGS
 336
 346 YVAFPEKQIGIVMLANKSYNPVREAVRILEKLO

1 match found in sequence:
 q48434 : EXTENDED SPECTRUM beta-lactamase precursor.
 (from "lactxs_spt.pep")
 TOIG of: q48434 check: 309 from: 1 to: 381

ID Q48434 PRELIMINARY; PRT; 381 AA.
 AC Q48434;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE EXTENDED SPECTRUM beta-lactamase precursor.
 GN bla_{CMY-2}.
 OS *Klebsiella pneumoniae*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Klebsiella*.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HEL-1;
 RX MEDLINE=96379897; PubMed=6787910;
 RA Baerentzen A., Stenplinger J., Jungwirth R., Giamarellos H.;
 RT "Characterization of the plasmidic beta-lactamase CMY-2, which is
 RT responsible for cephamycin resistance."
 RL Antimicrob. Agents Chemother. 40:221-224(1996).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-169;
 RA Dece D., Raakine L., Blancard H., Sanson-Le Pors M.J., Petit J.C.,
 RA Philpott A., Arlet G.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X91840; CA62957.1; -;
 DR EMBL: Y16784; CA676381.1; -;
 DR HSSP: P00811; 1C3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 381

SQ SEQUENCE 381 AA; 42003 MW; 8C30E62E52DFC311 CRC64;
 Q48434 Length: 381 March 17, 2003 12:32 Type: P Check: 309
 Found using 'KTXS' (swope073.key)

285 MYGIGMEMLNMPYDAKTVEGSDNKVALAPLPAVEVNPAPVAVKSWHKSTGSGFGS
 335
 345 YVAFPEKQIGIVMLANKSYNPVREAVRILEKLO

1 match found in sequence:
 q48435 : LAT-2 B-lactamase precursor.
 (from "lactxs_spt.pep")
 TOIG of: q48435 check: 9885 from: 1 to: 381

ID Q48435 PRELIMINARY; PRT; 381 AA.
 AC Q48435; 008034;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE LAT-2 B-lactamase precursor.
 GN bla_{LAT-2}.
 OS *Klebsiella pneumoniae*.
 OC plasmid pMEP.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Klebsiella*.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WILD N5;
 RA Gazouli M., Tzouveletis L.S., Pinarakis E., Miriagou V., Tzelepi E.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=96400699; PubMed=8807075;
 RA Gazouli M., Tzouveletis L.S., Pinarakis E., Miriagou V., Tzelepi E.;
 RT "Transferable cefoxitin resistance in enterobacteria from Greek
 RT hospitals and characterization of a plasmid-mediated group 1 beta-
 RT lactamase (LAT-2)."
 RL Antimicrob. Agents Chemother. 40:1736-1740(1996).
 DR EMBL: X97039; CA65752.1; -;
 DR EMBL: S83226; AAB46884.1; -;
 DR HSSP: P00811; 1C3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW plasmid; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 381
 SQ SEQUENCE 381 AA; 42036 MW; ED951747D7597B6A CRC64;
 Q48435 Length: 381 March 17, 2003 12:32 Type: P Check: 9885
 Found using 'KTXS' (swope073.key)

285 MYGIGMEMLNMPYDAKTVEGSDNKVALAPLPAVEVNPAPVAVKSWHKSTGSGFGS
 335
 345 YVAFPEKQIGIVMLANKSYNPVREAVRILEKLO

2 matches found in sequence:
 q48437 : Beta-lactamase, class C.
 (from "lactxs_spt.pep")
 TOIG of: q48437 check: 7779 from: 1 to: 382

ID Q48437 PRELIMINARY; PRT; 382 AA.
 AC Q48437;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE beta-lactamase, class C.
 GN FOX.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA32;
 RX MEDLINE=95110083; PubMed=7811034;
 RA Gonzalez-Ileiza M., Perez-Diaz J.C., Ayala J., Casellas J.M.,
 RT Martinez-Beltran J., Bush K., Baquero F.;
 RT "Gene sequence and biochemical characterization of FOX-1 from
 RT Klebsiella pneumoniae, a new AmpC-type plasmid-mediated beta-lactamase
 RT with two molecular variants.";
 RL Antimicrob. Agents Chemother. 38:2150-2157(1994).
 DR EMBL: X77455; CAA54602.1; -.
 DR HSSP: P05364; 2BUT.
 DR InterPro: IPR001466; Beta_Lactamase.
 DR InterPro: IPR001586; Beta_Lactamase_C.
 DR Pfam: PF00144; beta-Lactamase; 1.
 DR PROSITE: PS00336; BETA-LACTAMASE_C; 1.
 DR PROSITE: PS00336; BETA-LACTAMASE_C; 1.
 SQ SEQUENCE 382 AA; 41191 MW; C2516320E9357E9F CRC64;

Q4837 Length: 382 March 17, 2003 12:32 Type: P Check: 7779
 Found using 'KTXS' (swope073.key)

196 SOTLPLKLGHTHYIOVPESATANTAYGYSKEDKPVRTPGVLAAYGKIGSDLLKE
 246
 256 TEANMGYGDAAKTRIALTHGTGYSVGDMTQGLGWESYAPLPTQALLAGNSPAVSFOA
 335
 316 NPVTRAVKAMGEORLYNKSTGSGFAYVAFVAPARGIATVLANRNPTEARVKAHAA
 335
 376 ILSQLAE

 1 match found in sequence:
 q48443 ; Beta-lactamase precursor.
 (from "lactxs_spt.pep")
 TOIG of: q48443 check: 488 from: 1 to: 381

ID Q48443 PRELIMINARY; PRT; 381 AA.
 AC Q48443;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE beta-lactamase precursor.
 GN BLAAT-1.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HID STRAIN P20;
 RX MEDLINE=95110098; PubMed=7811049;
 RA Tzouveleakis I.S., Tzelepi E., Mentis A.F.;
 RT "Nucleotide sequence of a plasmidic cephalosporinase gene (bla-LAT-1)
 RT found in Klebsiella pneumoniae.";
 RL Antimicrob. Agents Chemother. 38:2207-2209(1994).
 DR EMBL: X78117; CAA55007.1; -.
 DR HSSP: P00811; IC3B.

DR InterPro: IPR001466; Beta_Lactamase.
 DR InterPro: IPR001586; Beta_Lactamase_C.
 DR Pfam: PF00144; beta-Lactamase; 1.
 DR PROSITE: PS00336; BETA-LACTAMASE_C; 1.
 KW signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 381 MATURE BETA-LACTAMASE.
 SQ SEQUENCE 381 AA; 42047 MW; DEF01356A336E090 CRC64;

Q48443 Length: 381 March 17, 2003 12:32 Type: P Check: 488
 Found using 'KTXS' (swope073.key)

285 MYGLGEMLMWPLKADSIINGSDSKVALALPAVEVNPAPAVKASVYKSTGFGS
 335
 345 YVAFVEKNLGIWLANKSYPNPVKEAARILEKIQ

1 match found in sequence:
 q48790 ; Sepa protein.
 (from "lactxs_spt.pep")
 TOIG of: q48790 check: 1658 from: 1 to: 391

ID Q48790 PRELIMINARY; PRT; 391 AA.
 AC Q48790;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Sepa protein.
 GN SEPA.
 OS Bacteria monocytoenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 CC Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LO28;
 RA Campillo M.L., Perez-Diaz J.C.;
 RT "Sepa: Un nuevo gen de Listeria monocytoenes implicado en la
 RT separacion celular.";
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LO28;
 RA Mary Luz C.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X92423; CAA63151.1; -.
 DR InterPro: IPR001279; Blactamase-like.
 DR Pfam: PF00753; lactamase_B; 1.
 SQ SEQUENCE 391 AA; 44415 MW; F6878A1C35870511 CRC64;

Q48790 Length: 391 March 17, 2003 12:32 Type: P Check: 1658
 Found using 'KTXS' (swope073.key)

174 KVALIGPEGWEAAVSENIFAGNAMIRRAFYMGSRSLRSGELGVDAGLGTASKGMSL
 224

234 LAPNDTITFDHEKRVDCIEVEFLMAPNTAPSEHMYTPOFKL

2 matches found in sequence:
 q51578 ; Beta-lactamase precursor.
 (from "lactxs_spt.pep")
 TOIG of: q51578 check: 9990 from: 1 to: 382

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ID 051578      PRELIMINARY;      PRT;      382 AA.
AC 051578:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-lactamase precursor.
GN BLAMOX-1.
OS Klebsiella pneumoniae.
OC plasmid PMOX-1.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NU2936;
RX MEDLINE=94156189; PubMed=8112596;
RA Horii T., Arakawa Y., Ohta M., Sugiyama T., Wacharotayankun R.,
  Ito H., Kato N.;
RT "Characterization of a plasmid-borne and constitutively expressed
  blaMOX-1 gene encoding Ampc-type beta-lactamase.";
RL Gene 139:93-98(1994).
DR EMBL; D13304; BAA02563.2; -.
DR HSSP; P05364; 2BLT.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Plasmid; Signal.
FT SIGNAL. 1 23 POTENTIAL.
FT CHAIN 24 382 BETA-LACTAMASE.
SQ SEQUENCE 382 AA; 40768 MW; BC42459644D62482 CRC64;

```

Q51578 Length: 382 March 17, 2003 12:32 Type: P Check: 9990 ..
 Found using 'KTXS' (swope073.key)

```

199  EQTLPLGLGMHTYVNPVKQAMASYAYGSKEDKPIRVNPGMLADEAYGKITSADLLAF 1--1
259  VKANIGVDKALQQAISLTGKHGYSVGGMTGLGMSYAPVTEQTLLAGNSAKVILEA 249
319  NPTAAPRESGQVLEFKTSSNGFCAYVAFPARGIGIVMLANRNYPPIPAKVAHAHLLA 1--1
      335
379  OLAG
-----
1 match found in sequence:
Q52615 : Beta-lactamase precursor.
(from "lactxs_spt.pep")
TOIG of: Q52615 check: 1582 from: 1 to: 300
-----
ID 052615      PRELIMINARY;      PRT;      300 AA.
AC 052615:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Beta-lactamase precursor.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=94339110; PubMed=8060986;
RA Tamaki M., Nukaga M., Sawai T.;
RT "Replacement of serine 237 in class A beta-lactamase of Proteus
  vulgaris modifies its unique substrate specificity.";
RL Biochemistry 33:10200-10206(1994).

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DR EMBL; D29982; BAA06252.1; -.
DR HSSP; Q47066; 1BZA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Signal.
FT SIGNAL. 1 29 POTENTIAL.
FT CHAIN 30 300 BETA-LACTAMASE.
SQ SEQUENCE 300 AA; 32838 MW; BA16949F16E2E028 CRC64;

Q52615 Length: 300 March 17, 2003 12:32 Type: P Check: 1582 ..
Found using 'KTXS' (swope073.key)

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```

189  IMAKSLQALTLGLDALGOSQROQLVTMLKNTTGDSIKAGLPKHVYVGDRTGSGDYGTT 1--1
249  NDIAVIMPENHAPLLIVYFTQEQNAKYRKDIKAARIVYRKE 239

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2 matches found in sequence:
 Q54488 : Carbapenem-hydrolyzing beta-lactamase.
 (from "lactxs_spt.pep")
 TOIG of: Q54488 check: 7669 from: 1 to: 294

```

ID 054488      PRELIMINARY;      PRT;      294 AA.
AC 054488:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Carbapenem-hydrolyzing beta-lactamase.
GN SME-2.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S6;
RC Rasmussen B.A., Keeney D., Cohen C.;
RA "Carbapenem-hydrolyzing beta-lactamase, SME-2.";
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S6;
RX MEDLINE=94379777; PubMed=8092824;
RA Naas T., Vandel L., Sougakoff W., Livermore D.M., Nordmann P.;
RT "Cloning and sequence analysis of the gene for a carbapenem-
  hydrolyzing class A beta-lactamase, SME-1, from Serratia marcescens
  S6.";
RL Antimicrob. Agents Chemother. 38:1262-1270(1994).
DR EMBL; U60295; AAB03414.1; -.
DR HSSP; P52663; 1BUU.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
SQ SEQUENCE 294 AA; 32246 MW; C326C0DC65293094 CRC64;

```

Q54488 Length: 294 March 17, 2003 12:32 Type: P Check: 7669 ..
 Found using 'KTXS' (swope073.key)

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1  MSNKNVNFSTASFVSVCLASAFNAHANKSDAAAKOIKRLIEDFDGRIGVFAIDTGGNT 1--1
61  F 8 11

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...
188      KAVANSKLKALGNVAKKAIYONWLGKNTGDARIRASVPADWVGDGTGSGAYGT
      238
248      ANDYAVMPKRNAPLIVSYITRKSCKDKHSDKTIASRIAIO
      238
...
1 match found in sequence:
q59276 : Beta-lactamase precursor (EC 3.5.2.6).
(from "lactixs_spt.pep")
TOIG of: q59276 check: 730 from: 1 to: 381

ID   Q59276      PRELIMINARY;      PRT;      381 AA.
AC   Q59276;
DT   01-NOV-1996 (TREMBLrel. 01, Created)
DR   01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE   01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DN   Beta-lactamase precursor (EC 3.5.2.6).
OS   BLAC.
OC   Citrobacter freundii.
CC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CX   NCBI_TaxID=546;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GN346;
RA   Tsukamoto K., Tachibana K., Yamazaki N., Ishii Y., Ujii K.,
RA   Nishida N., Sawai T.;
RT   "Role of lysine-67 in the active site of class C beta-lactamase from
RT   Citrobacter freundii GN346."
RL   Eur. J. Biochem. 188:15-22(1990).
DR   EMBL; D13207; BAA02494.1; -.
DR   HSSP; P00811; IC3B.
DR   InterPro; IPR001466; Beta_lactamase.
DR   InterPro; IPR001586; Beta_lactamase_C.
DR   Pfam; PF00144; beta_lactamase; 1.
DR   PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW   Hydrolyase; Signal.
FT   SIGNAL      1      20
FT   CHAIN       21     381
FT   SEQUENCE   381 AA; 42013 MW; E949AC92F314F338 CRC64;
SQ
O59276 Length: 381 March 17, 2003 12:32 Type: P Check: 730 ..
Found using 'KTXS' (swope073.key)

...
1 match found in sequence:
q59276 : Beta-lactamase precursor (EC 3.5.2.6).
(from "lactixs_spt.pep")
TOIG of: q59276 check: 730 from: 1 to: 381

ID   Q59276      PRELIMINARY;      PRT;      381 AA.
AC   Q59276;
DT   01-NOV-1996 (TREMBLrel. 01, Created)
DR   01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE   01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DN   Beta-lactamase precursor (EC 3.5.2.6).
OS   BLAC.
OC   Citrobacter freundii.
CC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CX   NCBI_TaxID=546;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GN346;
RA   Tsukamoto K., Tachibana K., Yamazaki N., Ishii Y., Ujii K.,
RA   Nishida N., Sawai T.;
RT   "Role of lysine-67 in the active site of class C beta-lactamase from
RT   Citrobacter freundii GN346."
RL   Eur. J. Biochem. 188:15-22(1990).
DR   EMBL; D13207; BAA02494.1; -.
DR   HSSP; P00811; IC3B.
DR   InterPro; IPR001466; Beta_lactamase.
DR   InterPro; IPR001586; Beta_lactamase_C.
DR   Pfam; PF00144; beta_lactamase; 1.
DR   PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW   Hydrolyase; Signal.
FT   SIGNAL      1      20
FT   CHAIN       21     381
FT   SEQUENCE   381 AA; 42013 MW; E949AC92F314F338 CRC64;
SQ
O59276 Length: 381 March 17, 2003 12:32 Type: P Check: 730 ..
Found using 'KTXS' (swope073.key)

...
1 match found in sequence:
q59401 : Class C beta-lactamase precursor (EC 3.5.2.6).
(from "lactixs_spt.pep")
TOIG of: q59401 check: 2391 from: 1 to: 384

ID   Q59401      PRELIMINARY;      PRT;      384 AA.
AC   Q59401;
DT   01-NOV-1996 (TREMBLrel. 01, Created)
DR   01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE   01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DN   Class C beta-lactamase precursor (EC 3.5.2.6).
OS   Enterobacter cloacae.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CX   Enterobacter.
CX   NCBI_TaxID=550;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GCI;
RA   MEDLINE=95197591; PubMed=7890700;
RA   Nukaga M., Haruta S., Tanimoto K., Kogure K., Taniguchi K., Tamaki M.,
RA   Sawai T.;
RT   "Molecular evolution of a class C beta-lactamase extending its
RT   substrate specificity."
RL   J. Biol. Chem. 270:5729-5735(1995).
DR   EMBL; D44479; BAA07922.1; -.
DR   HSSP; P05364; 2BLT.
DR   InterPro; IPR001466; Beta_lactamase.
DR   InterPro; IPR001586; Beta_lactamase_C.
DR   Pfam; PF00144; beta_lactamase; 1.
DR   PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW   Hydrolyase; Signal.
FT   SIGNAL      1      20
FT   CHAIN       21     384
FT   SEQUENCE   384 AA; 41612 MW; B3BC13B02531372F CRC64;
SQ
O59401 Length: 384 March 17, 2003 12:32 Type: P Check: 2391 ..
Found using 'KTXS' (swope073.key)

...
1 match found in sequence:
q59401 : Class C beta-lactamase precursor (EC 3.5.2.6).
(from "lactixs_spt.pep")
TOIG of: q59401 check: 2391 from: 1 to: 384

ID   Q59401      PRELIMINARY;      PRT;      384 AA.
AC   Q59401;
DT   01-NOV-1996 (TREMBLrel. 01, Created)
DR   01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE   01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DN   Class C beta-lactamase precursor (EC 3.5.2.6).
OS   Enterobacter cloacae.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CX   Enterobacter.
CX   NCBI_TaxID=550;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GCI;
RA   MEDLINE=95197591; PubMed=7890700;
RA   Nukaga M., Haruta S., Tanimoto K., Kogure K., Taniguchi K., Tamaki M.,
RA   Sawai T.;
RT   "Molecular evolution of a class C beta-lactamase extending its
RT   substrate specificity."
RL   J. Biol. Chem. 270:5729-5735(1995).
DR   EMBL; D44479; BAA07922.1; -.
DR   HSSP; P05364; 2BLT.
DR   InterPro; IPR001466; Beta_lactamase.
DR   InterPro; IPR001586; Beta_lactamase_C.
DR   Pfam; PF00144; beta_lactamase; 1.
DR   PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW   Hydrolyase; Signal.
FT   SIGNAL      1      20
FT   CHAIN       21     384
FT   SEQUENCE   384 AA; 41612 MW; B3BC13B02531372F CRC64;
SQ
O59401 Length: 384 March 17, 2003 12:32 Type: P Check: 2391 ..
Found using 'KTXS' (swope073.key)

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Found using 'KTXS' (swope073.key)

288 MYOGLWEMLNWPEVANTVYEGSDSKVALAPLPAEVENPPAPPYKASWYKKTGSTGFGS
338

348 YVAFPEKQIGIVMLANTSYNPAPRAVEAAYHLEALQ

2 matches found in sequence:

q8r7h7 : Predicted hydrolases of metallo-beta-lactamase fold.

(from "lacks_spt.pep")

TOIG of: q8r7h7 check: 3617 from: 1 to: 308

ID Q8R7H7 PRELIMINARY; PRT; 308 AA.
AC Q8R7H7;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Predicted hydrolases of metallo-beta-lactamase fold.
GN COMEC2 OR TTE2430.
OS Thermomanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermomanaerobacteriales; Thermomanaerobacteriaceae; Thermomanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013185; AAM25566.1; -;
KW Hydrolase; Complete proteome.
SQ SEQUENCE 308 AA; 33964 MW; 837BF3EDEL1A4D7A CRC64;

Q8R7H7 Length: 308 March 17, 2003 12:32 Type: P Check: 3617 ..
Found using 'KTXS' (swope073.key)

24 SFPSEFSNOKSYDSTITDNQCLPAISSEDSKLTVSFIDVGQSDSIFIKTPTSDKTMLI
74 77

84 DAGTPENGERVVNYIKQGVKIDVLVGTGPHPHDHIIGLPEV1Q

250 EVRPKIVAVISCGKNNYGHPHGETLEKLSGLITVYRTDECGTIIVAVSDKTVSFFRIK
300

1 match found in sequence:

q8rk40 : Beta-lactamase class A (EC 3.5.2.6).

(from "lacks_spt.pep")

TOIG of: q8rk40 check: 2975 from: 1 to: 289

ID Q8RK40 PRELIMINARY; PRT; 289 AA.
AC Q8RK40;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta-lactamase class A (EC 3.5.2.6).
GN P. ALC-A.
OS Providencia alcalifaciens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Providencia.

OX NCBI_TaxID=126385;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PSL199;

RA Beauchef-Havard A., Arlet G., Philippou A.;

RT "A new class A beta-lactamase in an atypical strain of Providencia

alcalifaciens.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ438771; CAD27491.1; -;

KW Hydrolase.

SQ SEQUENCE 289 AA; 32007 MW; CD0F7AFEC17939C0 CRC64;

Q8RK40 Length: 289 March 17, 2003 12:32 Type: P Check: 2975 ..
Found using 'KTXS' (swope073.key)

1 MTLRRTFAALILSPGLICICEDFTGSRSLNKKRVGLVCPFKPPDDKTINGNOR
51 54

61 PPLDSTVKSINACANVLAKVDKKLSHSMIVTEKNIVTSPVA

1 match found in sequence:

q8rkbl : Beta-lactamase class A.

(from "lacks_spt.pep")

TOIG of: q8rkbl check: 8889 from: 1 to: 291

ID Q8RKBL PRELIMINARY; PRT; 291 AA.
AC Q8RKBL;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta-lactamase class A.
GN KLU6.
OS Kluysera ascorbata.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Kluysera.
OX NCBI_TaxID=51288;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 15-79;
RA Humeniuk C., Arlet G., Labia R., Grimont P., Philippou A.;
RT "Beta-lactamase of Kluysera ascorbata: progenitor of some plasmid-
encoded CRX-M types.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ427464; CAD20588.3; -;
SQ SEQUENCE 291 AA; 31362 MW; 82E70C78D30DFC80 CRC64;

Q8RKBL Length: 291 March 17, 2003 12:32 Type: P Check: 8889 ..
Found using 'KTXS' (swope073.key)

187 LMAOGLKMLTGKALAETORAQVLTWLGKNTGSASIRAGLPSWGVGDYTGSDYGT
237

247 NDIATVWPNHAPDIVLYTYFTPEQKASRRDYLAAAKIYTHG

1 match found in sequence:

q8rl89 : Beta-lactamase (Fragment).

(from "lacks_spt.pep")

TOIG of: q8rl89 check: 8113 from: 1 to: 388

ID Q8RL89 PRELIMINARY; PRT; 388 AA.
AC Q8RL89;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Beta-lactamase (Fragment).
 GN AMPc.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CF001810;
 RA De Champs C., Poirol L., Bonnet R., Sirot D., Chanal C., Sirot J.,
 RA Nordmann P.;
 RT "Prospective survey of beta-lactamases produced by ceftazidime-
 RT resistant Pseudomonas aeruginosa isolated in a French hospital in
 RT 2000.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY083594; AAM08944.1; -.
 FT NON_TER 1
 SQ SEQUENCE 388 AA; 42294 MW; 7DE7268B4284BFC5 CRC64;

Q8RL89 Length: 388 March 17, 2003 12:32 Type: P Check: 8113 ..
 Found using 'KTXS' (swope073.key)

283 MTGGLGWEAYDWPISLRKLGAGNSTPMALQPHRIARLPAPQALGEGRLNKTGSTNGFGA
 333
 343 YVAFVPGRDGLVILANRNPNAERVKIAYAILSGLEQOGKVPPL

1 match found in sequence:
 q8rl90 ; Beta-lactamase.
 (from "lactxs_spt.pep")
 TOIG of: q8rl90 check: 8212 from: 1 to: 397

ID Q8RL90 PRELIMINARY; PRT; 397 AA.
 AC Q8RL90;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Beta-lactamase.
 GN AMPc.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CF001610;
 RA De Champs C., Poirol L., Bonnet R., Sirot D., Chanal C., Sirot J.,
 RA Nordmann P.;
 RT "Prospective survey of beta-lactamases produced by ceftazidime-
 RT resistant Pseudomonas aeruginosa isolated in a French hospital in
 RT 2000.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY083593; AAM08943.1; -.
 SQ SEQUENCE 397 AA; 43343 MW; 8514A66B614C07DB CRC64;

Q8RL90 Length: 397 March 17, 2003 12:32 Type: P Check: 8212 ..
 Found using 'KTXS' (swope073.key)

292 MTGGLGWEAYDWPISLRKLGAGNSTPMALQPHRIARLPAPQALGEGRLNKTGSTNGFGA
 342
 352 YVAFVPGRDGLVILANRNPNAERVKIAYAILSGLEQOGKVPPL

1 match found in sequence:
 q8rl91 ; Beta-lactamase.
 (from "lactxs_spt.pep")
 TOIG of: q8rl91 check: 7894 from: 1 to: 397

ID Q8RL91 PRELIMINARY; PRT; 397 AA.
 AC Q8RL91;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Beta-lactamase.
 GN AMPc.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CF001710;
 RA De Champs C., Poirol L., Bonnet R., Sirot D., Chanal C., Sirot J.,
 RA Nordmann P.;
 RT "Prospective survey of beta-lactamases produced by ceftazidime-
 RT resistant Pseudomonas aeruginosa isolated in a French hospital in
 RT 2000.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY083592; AAM08942.1; -.
 SQ SEQUENCE 397 AA; 43385 MW; B383F356154AF91E CRC64;

Q8RL91 Length: 397 March 17, 2003 12:32 Type: P Check: 7894 ..
 Found using 'KTXS' (swope073.key)

292 MTGGLGWEAYDWPISLRKLGAGNSTPMALQPHRIARLPAPQALGEGRLNKTGSTNGFGA
 342
 352 YVAFVPGRDGLVILANRNPNAERVKIAYAILSGLEQOGKVPPL

1 match found in sequence:
 q8rla6 ; Beta-lactamase OXA-33.
 (from "lactxs_spt.pep")
 TOIG of: q8rla6 check: 1882 from: 1 to: 275

ID Q8RLA6 PRELIMINARY; PRT; 275 AA.
 AC Q8RLA6;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Beta-lactamase OXA-33.
 GN BUAOXA-33.
 OS Acinetobacter baumannii.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acinetobacter.
 OX NCBI_TaxID=470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Silva G.-J., Bertolo E., Correia M., Duarte A., Peixe L.;
 RT "First isolation of a new class D beta-lactamase, OXA-33, in a
 RT clinical isolate of Acinetobacter baumannii from Portugal.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY082394; AAL92496.1; -.
 SQ SEQUENCE 275 AA; 30939 MW; 5FAE27A6A1ABC62B CRC64;

Q8RLA6 Length: 275 March 17, 2003 12:32 Type: P Check: 1882 ..
 Found using 'KTXS' (swope073.key)

1 MKKFLPFISILVSLACSSIKTSEDNPHISSQOHEKAISYFDEAQTQGVIIKEG
24 27

61 KNLSTYGNALARANKEY

1 match found in sequence:
q8rlk8 ; Beta-lactamase CTX-M-22.
(from "lactxs_spt.pep")
TOIG of: q8rlk8 check: 346 from: 1 to: 291

ID Q8RLK8 PRELIMINARY; PRT; 291 AA.
AC Q8RLK8;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Beta-lactamase CTX-M-22.
GN BLACTX-M-22
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu Y., Wei Z., Zhou W., Zhou Z., Shen P., Chen Y.;
RT "A novel beta-lactamase CTX-M-22 isolated from Klebsiella pneumoniae
in Zhejiang Province, China."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY080894; AAL86924.1;
SQ SEQUENCE 291 AA; 31200 MW; 49C7742A61F07BA4 CRC64;

Q8RLK8 Length: 291 March 17, 2003 12:32 Type: P Check: 346
Found using 'KTXS' (swope073.key)

187 RAMOITLNLTLGKALGDSORALVTWKKNTGASTQAGLPASWVGKGTSGDYGT
237

247 NDIAVWPKDRAPLIVYFTQPOKAESESRDVLASAKIVTNG

1 match found in sequence:

q8rmb8 ; Beta-lactamase JOHN-1.
(from "lactxs_spt.pep")
TOIG of: q8rmb8 check: 8628 from: 1 to: 248

ID Q8RMB8 PRELIMINARY; PRT; 248 AA.
AC Q8RMB8;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Beta-lactamase JOHN-1.
GN BLAJOHN-1.
OS Cytophaga johnsonae.
OC Bacteria; CFb group; Flavobacteriia; Flavobacteriaceae; Flavobacterium.
OX NCBI_TaxID=986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CIP100931;
RA Naas T., Bellais S., Nordmann P.;
RT "Molecular and biochemical characterization of JOHN-1, a new class B
carbapenem-hydrolyzing beta-lactamase";
RL Antimicrob. Agents Chemother. 0:0-0(2001).
DR EMBL; AY028464; AAK38324.1;
SQ SEQUENCE 248 AA; 28075 MW; 055884623892B692 CRC64;

Q8RMB8 Length: 248 March 17, 2003 12:32 Type: P Check: 8628
Found using 'KTXS' (swope073.key)

64 LFPDAPWKTQFQPLDLSIKAKHNKEVYMLFTHSHEDRAGCFDYKKKGKIKYISIKLTD
114

124 ILKKKPEPRAEFLISMDTTFYGNHTEFYYYPKGAHPNDIVAM

1 match found in sequence:
q8rml0 ; AmpC.
(from "lactxs_spt.pep")
TOIG of: q8rml0 check: 218 from: 1 to: 381

ID Q8RML0 PRELIMINARY; PRT; 381 AA.
AC Q8RML0;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE AmpC.
GN AmpC.
OS Citrobacter werkmanii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=67827;
RN [1]
RP SEQUENCE FROM N.A.
RA Naas T., Aubert D., Fortineau N., Nordmann P.;
RT "Cloning and sequencing of five genes encoding AmpC beta-lactamase and
their regulator genes from Citrobacter braakii, Citrobacter murliniae,
RT Citrobacter werkmanii, Escherichia fergusonii and Enterobacter
RT cancerogenus.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF492448; AAM11670.1;
SQ SEQUENCE 381 AA; 41978 MW; FE5E048364B49857 CRC64;

Q8RML0 Length: 381 March 17, 2003 12:32 Type: P Check: 218
Found using 'KTXS' (swope073.key)

285 MYOGLGEMLNMPVADSIINGSKVALALPRAVEVNPAPARAKASWYHKGTSGFGS
335

345 YVAFVPEKNLGIYMLANKSYPNPARYDAWRIILEKLQ

1 match found in sequence:
q8rml2 ; AmpC.
(from "lactxs_spt.pep")
TOIG of: q8rml2 check: 1086 from: 1 to: 381

ID Q8RML2 PRELIMINARY; PRT; 381 AA.
AC Q8RML2;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE AmpC.
GN AmpC.
OS Citrobacter braakii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=57706;
RN [1]
RP SEQUENCE FROM N.A.
RA Naas T., Aubert D., Fortineau N., Nordmann P.;
RT "Cloning and sequencing of five genes encoding AmpC beta-lactamase and

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RT their regulator genes from Citrobacter braakii, Citrobacter murliniae,
RT Citrobacter werkmanii, Escherichia fergusonii and Enterobacter
RT cancerogenus."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF492447; AAM11668.1; C72115D6462B3CF CRC64;
SQ SEQUENCE 381 AA; 41929 MW; C72115D6462B3CF CRC64;

O8RML2 Length: 381 March 17, 2003 12:32 Type: P Check: 1086 ..
Found using 'KTXS' (swope073.key)

...

285 MYOGLGWEMLNMPVKADSIISGSDSKVLAALPAVEVNPAPVAVKASVWVKSTGSGFGS
335
345 YVAFPEKNLGIIVMLANKSYNPAPVAVKAAWRIELKQ

-----
1 match found in sequence:
q8rm14 : Ampc.
(from "lactxs_spt.pep")
TOIG of: q8rm14 check: 4995 from: 1 to: 381

ID O8RML4 PRELIMINARY; PRT; 381 AA.
AC O8RML4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ampc.
GN Ampc.
OS Enterobacter cancerogenus.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=69218;
RN [1]
RP SEQUENCE FROM N.A.
RA Naas T., Aubert D., Fortineau N., Nordmann P.;
RT Cloning and sequencing of five genes encoding Ampc beta-lactamase and
RT their regulator genes from Citrobacter braakii, Citrobacter murliniae,
RT Citrobacter werkmanii, Escherichia fergusonii and Enterobacter
RT cancerogenus."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF492446; AAM11666.1;
SQ SEQUENCE 381 AA; 41357 MW; ACB32217AEDAC11C CRC64;

O8RML4 Length: 381 March 17, 2003 12:32 Type: P Check: 4995 ..
Found using 'KTXS' (swope073.key)

...

285 MYOGLGWEMLNMPVDGKTIIDSDNKIALALPAVEVNPAPVAVKASVWVKSTGSGFGS
335
345 YVAFPEKOLGIIVMLANKSYNPAPVAVKAAWRIELKQ

-----
1 match found in sequence:
q8rm16 : Ampc.
(from "lactxs_spt.pep")
TOIG of: q8rm16 check: 711 from: 1 to: 381

ID O8RML6 PRELIMINARY; PRT; 381 AA.
AC O8RML6;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ampc.
GN Ampc.
OS Citrobacter murliniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.

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OX NCBI_TaxID=67829;
RN [1]
RP SEQUENCE FROM N.A.
RA Naas T., Aubert D., Fortineau N., Nordmann P.;
RT Cloning and sequencing of five genes encoding Ampc beta-lactamase and
RT their regulator genes from Citrobacter braakii, Citrobacter murliniae,
RT Citrobacter werkmanii, Escherichia fergusonii and Enterobacter
RT cancerogenus."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF492445; AAM11664.1;
SQ SEQUENCE 381 AA; 42107 MW; C8CE1A21711DF765 CRC64;

O8RML6 Length: 381 March 17, 2003 12:32 Type: P Check: 711 ..
Found using 'KTXS' (swope073.key)

...

285 MYOGLGWEMLNMPVKADIVINGSDSKIALALPAVEVNPAPVAVKASVWVKSTGSGFGS
335
345 YVAFPEKNLGIIVMLANKSYNPAPVADAWRIELKQ

-----
1 match found in sequence:
q8rm1 : Cephalosporinase.
(from "lactxs_spt.pep")
TOIG of: q8rm1 check: 7600 from: 1 to: 397

ID O8RMP1 PRELIMINARY; PRT; 397 AA.
AC O8RMP1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cephalosporinase.
GN Ampc.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RA De Champs C., Poirol L., Bonnet R., Sirot D., Chanal C., Sirot J.,
RT "Prospective survey of beta-lactamase produced by ceftazidime-
RT resistant Pseudomonas aeruginosa isolated in a French hospital in
RT 2000."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF490770; AAM08410.1;
SQ SEQUENCE 397 AA; 43399 MW; B383F356154AFCE CRC64;

O8RMP1 Length: 397 March 17, 2003 12:32 Type: P Check: 7600 ..
Found using 'KTXS' (swope073.key)

...

292 MYOGLGWEAYDWPISLKLQAGNSTPMALOPHRIARLAPDALEGORLLNKTSTGFGA
342
352 YVAFVPGDGLVILANRNPNAERVKIAVAIILSGEQAKVPL

-----
1 match found in sequence:
q8rmw4 : CTX-M type beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q8rmw4 check: 1053 from: 1 to: 291

ID O8RMW4 PRELIMINARY; PRT; 291 AA.
AC O8RMW4;

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DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE CTX-M type beta-lactamase.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=164;
 RA Stuenkelburg E., Feucht H., Laufs R.;
 RT "Escherichia coli clinical strain 164 CTX-M type beta-lactamase."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF48377; AAL99990.1; --
 SO SEQUENCE 291 AA; 31232 MW; B02DD551D87EFBE8 CRC64;

Q8RMA4 Length: 291 March 17, 2003 12:32 Type: P Check: 1053
 Found using 'KTXS' (swope073.key)

187 RAMAQTILNLTGKALGDSQRAQLVTWMMKNTGASIQAGLPASWYVGDYGTG
 237
 247 NDIAVWPGRAPLILVTYFTQPOPKAESRDVILASAKIYTN

 1 match found in sequence:
 q8rna0 : Extended-spectrum beta-lactamase CTX-M-9 (Fragment).
 (from "lactxs_spt.pep")
 TOIG of: q8rna0 check: 6124 from: 1 to: 264

ID Q8RNA0 PRELIMINARY; PRT; 264 AA.
 AC Q8RNA0:
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Extended-spectrum beta-lactamase CTX-M-9 (Fragment).
 GN BLACTX-M-9.
 OS Escherichia coli.
 OC Plasmid pSUN-7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lu J., Tang Y.C., Wu B.Q., Zhang K.X., Zhu J.X., Tan S.Q., Bi X.G.;
 RT "Plasmid-mediated extended-spectrum beta-lactamase CTX-M-9 in
 RT Escherichia coli in China."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF484965; AAL91566.1; --
 KW Plasmid.
 FT NON_TER 1 1
 DE 264 264
 SO SEQUENCE 264 AA; 27985 MW; 90E436D59C520E2 CRC64;

Q8RNA0 Length: 264 March 17, 2003 12:32 Type: P Check: 6124
 Found using 'KTXS' (swope073.key)

182 RAMAQTILNLTGKALGDSQRAQLVTWMMKNTGASIRAGLPASWYVGDYGTG
 232
 242 NDIAVWPGRAPLILVTYFTQPOPKAESRDVILASAKIYTN

 2 matches found in sequence:

q8rt61 : Class A beta-lactamase CFXA3 (Fragment).
 (from "lactxs_spt.pep")
 TOIG of: q8rt61 check: 8025 from: 1 to: 315

ID Q8RT61 PRELIMINARY; PRT; 315 AA.
 AC Q8RT61:
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Class A beta-lactamase CFXA3 (Fragment).
 GN CFXA3.
 OS Capnocytophaga ochracea.
 OC Bacteria; CFB group; Flavobacteriia; Flavobacteriaceae; Capnocytophaga.
 NCBI_TaxID=1018;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jolivet-Gougeon A., Desbordes L., Tamaoui-Shacoori Z., Sixou J.-L.,
 RA Bonnaure-Mallet M., Burgaraeve N., Cormier M.;
 RT "Partial genetic and biochemical analysis of an Ambler class A
 RT extended-spectrum beta-lactamase from Capnocytophaga ochracea."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF472622; AAL79549.1; --
 FT NON_TER 1 1
 SO SEQUENCE 315 AA; 34541 MW; 079F2598C3B503AD CRC64;

Q8RT61 Length: 315 March 17, 2003 12:32 Type: P Check: 8025
 Found using 'KTXS' (swope073.key)

62 ROTVKNKSVYPMMSVFKVHQAALCNDPDKGSLDTLVNINRDKLPKTSPLRDY
 112
 122 SCPVISLTVRDLRLRYLTQSDNNASNLAKKDMVNVVQDTSFAT
 198 AAMLNRLFTGLIDDEKOSFKNTLKECKTGVDRIAPLDEKGVYLAHKTSDDVEN
 248
 258 GVLAAHNDVAYICLPNNISYTLAVFYKDEKGNESQASQYVAHIS

 1 match found in sequence:
 q8rtf9 : Extended-spectrum beta-lactamase CTX-M-13 (Fragment).
 (from "lactxs_spt.pep")
 TOIG of: q8rtf9 check: 6798 from: 1 to: 264

ID Q8RTF9 PRELIMINARY; PRT; 264 AA.
 AC Q8RTF9:
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Extended-spectrum beta-lactamase CTX-M-13 (Fragment).
 GN BLACTX-M-13.
 OS Enterobacter cloacae.
 OC Plasmid pSUN-7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUN-115;
 RA Lu J., Tang Y.C., Wu B.Q., Zhang K.X., Zhu J.X., Tan S.Q., Bi X.G.;
 RT "Plasmid-mediated extended-spectrum beta-lactamase CTX-M-13 in
 RT Enterobacter cloacae in China."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF462399; AAL77985.1; --
 KW Plasmid.


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FT  NON_TER      1      1
FT  NON_TER      264    264
SQ  SEQUENCE      264 AA; 28160 MW; BF13E416E72A8636 CRC64;
Q8RTF9 Length: 264 March 17, 2003 12:32 Type: P Check: 6798
Found using 'KTXS' (swope073.key)

...

182  RAMOQLTQNLIGHALGETORQALVTWIKGNTGASTIRAGLPTSWYGDYSGDYGTT
232
242  NDIAVIMPOGRAPLVLTVTYTPQ

-----
1 match found in sequence:
g8rtg0 ; Extended-spectrum beta-lactamase CTX-M-14 (Fragment).
(from "lactxs_spt.pep")
TOIG of: g8rtg0 check: 6145 from: 1 to: 264

ID  Q8RTG0      PRELIMINARY; PRT; 264 AA.
AC  Q8RTG0:
DT  01-JUN-2002 (TREMBLrel. 21, Created)
DT  01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE  01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE  Extended-spectrum beta-lactamase CTX-M-14 (Fragment).
GN  BLACTX-M-14.
OS  Serratia liquefaciens.
OG  Plasmid pSUN-8.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Serratia.
OX  NCBI_TaxID=614;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=SUB-188;
RA  Lu J., Tang Y.C., Wu B.Q., Zhang K.X., Zhu J.X., Tan S.Q., Bi X.G.;
RT  "Plasmid-mediated extended-spectrum beta-lactamase CTX-M-14 in
RL  Serratia liquefaciens in China.";
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF462396; AAL77984.1; -.
KW  Plasmid.
FT  NON_TER      1      1
FT  NON_TER      264    264
SQ  SEQUENCE      264 AA; 28013 MW; 90E436CB7C2B30E2 CRC64;
Q8RTG0 Length: 264 March 17, 2003 12:32 Type: P Check: 6145
Found using 'KTXS' (swope073.key)

...

182  RAMOQLTQNLIGHALGETORQALVTWIKGNTGASTIRAGLPTSWYGDYSGDYGTT
232
242  NDIAVIMPOGRAPLVLTVTYTPQ

-----
1 match found in sequence:
g8rt34 ; Metallo-beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: g8rt34 check: 5119 from: 1 to: 447

ID  Q8RT34      PRELIMINARY; PRT; 447 AA.
AC  Q8RT34:
DT  01-JUN-2002 (TREMBLrel. 21, Created)
DT  01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT  01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE  Metallo-beta-lactamase.
GN  MA0605.
OS  Methanosarcina acetivorans.
OC  Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC  Methanosarcinaceae; Methanosarcina.

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OX  NCBI_TaxID=2214;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C2A / ATCC 35395 / DSM 2834;
RX  MEDLINE=21929760; PubMed=11932238;
RA  Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,
RA  Fitzhugh W., Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
RA  Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA  Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA  Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA  Heederich R., Ingram-Smith C., Kuetlne H.C., Krzycki J.A.,
RA  Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA  Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA  Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA  Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA  Metcalf W.W., Birren B.;
RT  "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT  and physiological diversity.";
RL  Genome Res. 12:532-542(2002).
DR  EMBL; AE010721; AAM04049.1; -.
KW  Complete proteome.
SQ  SEQUENCE      447 AA; 49607 MW; 708CB30856596713 CRC64;
Q8RT34 Length: 447 March 17, 2003 12:32 Type: P Check: 5119
Found using 'KTXS' (swope073.key)

...

165  PAGAVIYACDFKIDRPTMGAPDFRFSLKGVIAMITESTNMGRSKPTPSEOIAND
215
225  MVRDVLGTEDSDVGMITTFASHIARLKAIIIEAEMGRIPVL

-----
1 match found in sequence:
g8txa0 ; Predicted hydrolase of the metallo-beta-lactamase superfamily.
(from "lactxs_spt.pep")
TOIG of: g8txa0 check: 397 from: 1 to: 453

ID  Q8TXA0      PRELIMINARY; PRT; 453 AA.
AC  Q8TXA0:
DT  01-JUN-2002 (TREMBLrel. 21, Created)
DT  01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE  01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE  Predicted hydrolase of the metallo-beta-lactamase superfamily.
GN  MK0775.
OS  Methanopyrus kandleri.
OC  Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC  Methanopyrus.
OX  NCBI_TaxID=2320;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=AV19 / DSM 6324 / JCM 9639;
RX  MEDLINE=21927647; PubMed=11930014;
RA  Slesarev A.I., Mezhevaaya K.V., Makarova K.S., Polushin N.N.,
RA  Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA  Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA  Malysk A.G., Koonin E.V., Kozayavkin S.A.;
RT  "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT  and monophyly of archaeal methanogens.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR  EMBL; AE010369; AAM01989.1; -.
KW  Hydrolase; Complete proteome.
SQ  SEQUENCE      453 AA; 50760 MW; 099898A0C9CC54CA CRC64;
Q8TXA0 Length: 453 March 17, 2003 12:32 Type: P Check: 397
Found using 'KTXS' (swope073.key)

...

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Q8VKZ0 Length: 372 March 17, 2003 12:32 Type: P Check: 7371 ..
Found using 'KTXS' (swope073.key)

284 MYGIGWEMLNMPVDKTYVDGSDNKKVALAPLPAEYVNPAPPYKASWVHKGTGTGSGFGS
334

344 YVAFIPKQIGIVMLANKSTPNPRLVETA

1 match found in sequence:

q8vkz1 ; Beta-lactamase.
(from "lactxs_spt.pep")

TOIG of: q8vkz1 check: 8607 from: 1 to: 381

ID Q8VKZ1 PRELIMINARY; PRT; 381 AA.

AC Q8VKZ1;

DT 01-MAR-2002 (TREMblrel. 20, Created)

DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Beta-lactamase.

GN AMPC.

OS Enterobacter hormaechei.

OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Enterobacter.

OX NCBI_TaxID=158836;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CIP 103441T;

RA Rottman M.M., Benzerara L., Hanau B., Arlet G.;

RT "Variability of the ampC gene among species belonging to genus

RT Enterobacter."

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ311364; CAC85357.1; -

DR InterPro: IPR001466; Beta_lactamase.

DR InterPro: IPR001586; Beta_lactamase_C.

DR Pfam: PF00144; beta-lactamase_1.

DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.

SQ SEQUENCE 381 AA; 41444 MW; 3852D04B9F237BA0 CRC64;

Q8VKZ1 Length: 381 March 17, 2003 12:32 Type: P Check: 8607 ..
Found using 'KTXS' (swope073.key)

...

285 MYGIGWEMLNMPVEAKTVIEGSDNKKVALAPLPAEYVNPAPPYKASWVHKGTGTGSGFGS
335

345 YVAFIPKQIGIVMLANKSTPNPRLVETA

1 match found in sequence:

q8vkz2 ; AmpC beta-lactamase.
(from "lactxs_spt.pep")

TOIG of: q8vkz2 check: 2566 from: 1 to: 381

ID Q8VKZ2 PRELIMINARY; PRT; 381 AA.

AC Q8VKZ2;

DT 01-MAR-2002 (TREMblrel. 20, Created)

DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE AmpC beta-lactamase.

GN AMPC.

OS Enterobacter asburiae.

OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Enterobacter.

OX NCBI_TaxID=61645;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CIP 103358 T;
RA Rottman M.M.;

RL Thesis (2001), Faculte de Medecine Necker-Enfants malades, Paris,

RL France. AJ311172; CAC85157.1; -

DR EMBL: AJ311172; CAC85157.1; -

DR InterPro: IPR001466; Beta_lactamase.

DR InterPro: IPR001586; Beta_lactamase_C.

DR Pfam: PF00144; beta-lactamase_1.

DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.

SQ SEQUENCE 381 AA; 41481 MW; 372056C66DB81D71 CRC64;

Q8VKZ2 Length: 381 March 17, 2003 12:32 Type: P Check: 2566 ..
Found using 'KTXS' (swope073.key)

...

285 MYGIGWEMLNMPVDKTYVDGSDNKKVALAPLPAEYVNPAPPYKASWVHKGTGTGSGFGS
335

345 YVAFIPKQIGIVMLANKSTPNPRLVETA

1 match found in sequence:

q8vn22 ; Beta-lactamase class A.
(from "lactxs_spt.pep")

TOIG of: q8vn22 check: 8451 from: 1 to: 291

ID Q8VN22 PRELIMINARY; PRT; 291 AA.

AC Q8VN22;

DT 01-MAR-2002 (TREMblrel. 20, Created)

DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Beta-lactamase class A.

GN KluA-11.

OS Kluysera ascorbata.

OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Kluysera.

OX NCBI_TaxID=51288;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=4450-94;

RA Humenik C., Arlet G., Labia R., Grimont P., Philippot A.;

RT "Beta-lactamase of Kluysera ascorbata: progenitor of some plasmid-

RT encoded CTX-M types."

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ427468; CAD20592.1; -

DR InterPro: IPR001466; Beta_lactamase.

DR InterPro: IPR000871; Beta_lactamase_A.

DR Pfam: PF00144; beta-lactamase; 1.

DR PRINTS: PR00118; BLACTAMASE.

DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.

SQ SEQUENCE 291 AA; 31383 MW; 86BE013CBA4A94F7 CRC64;

Q8VN22 Length: 291 March 17, 2003 12:32 Type: P Check: 8451 ..
Found using 'KTXS' (swope073.key)

...

187 LMAQTILNLTGLKALAEFGAQLVTLKNGTTGSASIQAGLPKSMWVYGDKGTGSDYDPT
237

247 THAIITPENHAPLVLYTYFTOPDQKAESRDVLAATAAKIYTHG

...

1 match found in sequence:

q8vn23 ; Beta-lactamase class A.
(from "lactxs_spt.pep")

TOIG of: q8vn23 check: 9371 from: 1 to: 291

```

ID Q8VN23 PRELIMINARY; PRT; 291 AA.
AC Q8VN23;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Beta-lactamase class A.
GN KLU-10.
OS Kluysvera ascorbata.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Kluysvera.
OX NCBI_TaxID=51288;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4350;
RA Humenluk C., Arlet G., Labia R., Grimont P., Philippou A.;
RT "beta-lactamase of Kluysvera ascorbata: progenitor of some plasmid-
  encoded CTX-M types."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ427467; CAD20591.1;
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
SQ SEQUENCE 291 AA; 31364 MW; 8F44D97C7EFE362 CRC64;

Q8VN23 Length: 291 March 17, 2003 12:32 Type: P Check: 9371 ..
Found using 'KTXS' (swope073.key)

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187 LAMAOTLKNLTLGKALAEFORAQLVTWLGKNTGTSASIRAGLPKSMVVGDKTSGDYGT
237

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247 NDIAIWPENHAPLVLTFTPTPEOKAESRRDVLAAAKIVTHG

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1 match found in sequence:
q8vn24 ; Beta-lactamase class A.
(from "lactxs_spt.pep")

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TOIG of: q8vn24 check: 9057 from: 1 to: 291

```

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ID Q8VN24 PRELIMINARY; PRT; 291 AA.
AC Q8VN24;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Beta-lactamase class A.
GN KLU-8.
OS Kluysvera ascorbata.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Kluysvera.
OX NCBI_TaxID=51288;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 3-89;
RA Humenluk C., Arlet G., Labia R., Grimont P., Philippou A.;
RT "beta-lactamase of Kluysvera ascorbata: progenitor of some plasmid-
  encoded CTX-M types."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ427465; CAD20589.1;
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
SQ SEQUENCE 291 AA; 31398 MW; 9B127ED3C1D2E7C0 CRC64;

Q8VN24 Length: 291 March 17, 2003 12:32 Type: P Check: 9057 ..
Found using 'KTXS' (swope073.key)

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```

187 LAMAOTLKNLTLGKALAEFORAQLVTWLGKNTGTSASIRAGLPKSMVVGDKTSGDYGT
237

```

```

247 NDIAIWPENHAPLVLTFTPTPEOKAESRRDVLAAAKIVTHG

```

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1 match found in sequence:
q8vn25 ; Beta-lactamase class A.
(from "lactxs_spt.pep")
TOIG of: q8vn25 check: 9211 from: 1 to: 291

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ID Q8VN25 PRELIMINARY; PRT; 291 AA.
AC Q8VN25;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Beta-lactamase class A.
GN KLU-5.
OS Kluysvera ascorbata.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Kluysvera.
OX NCBI_TaxID=51288;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 12-79;
RA Humenluk C., Arlet G., Labia R., Grimont P., Philippou A.;
RT "beta-lactamase of Kluysvera ascorbata: progenitor of some plasmid-
  encoded CTX-M types."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ427463; CAD20587.1;
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
SQ SEQUENCE 291 AA; 31341 MW; 9A2FPCACB735DCAB CRC64;

Q8VN25 Length: 291 March 17, 2003 12:32 Type: P Check: 9211 ..
Found using 'KTXS' (swope073.key)

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```

187 LAMAOTLKNLTLGKALAEFORAQLVTWLGKNTGTSASIRAGLPKSMVVGDKTSGDYGT
237

```

```

247 NDIAIWPENHAPLVLTFTPTPEOKAESRRDVLAAAKIVTHG

```

```

1 match found in sequence:
q8vn2 ; Beta lactamase (Fragment).
(from "lactxs_spt.pep")

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TOIG of: q8vn2 check: 4483 from: 1 to: 381

```

```

ID Q8VN2 PRELIMINARY; PRT; 381 AA.
AC Q8VN2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Beta lactamase (Fragment).
GN AMPc.
OS Enterobacter intermedium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=61648;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN-CIP 79.27r(AMCC 33110);
RA Rottman M.M., Benzerara L., Hanau B., Arlet G.;
RT "Variability of the ampC gene among species belonging to genus
   Enterobacter.";
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ311365; CAC85358.1; -.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.
FT NON_TER 1
FT SEQUENCE 381 AA; 41298 MW; 0DE390FB6759C792 CRC64;

O8VNM2 Length: 381 March 17, 2003 12:32 Type: P Check: 4483
Found using 'KTXS' (swope073.key)

...

284 MYGLGEMLMNPVDAKTVVNGSDNKLALALPKVNPAPPVKASVYHKTGSGFGS
334
344 YVAFIPKDLGITVMLANKSYNPAPVAYRRLSLAP
1--1
1 match found in sequence:
q8vnt7 ; Beta-lactamase (Fragment).
(from "lactxs_spt.pep")
TOIG of: q8vnt7 check: 3072 from: 1 to: 373

ID O8VNT7 PRELIMINARY; PRT; 373 AA.
AC O8VNT7;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Beta-lactamase (Fragment).
GN AMPc.
OS Enterobacter cancerogenus.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_Taxid=69218;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CIP103/87r;
RA Rottman M.M., Benzerara L., Hanau B., Arlet G.;
RT "Sequence variability of chromosomal ampC beta-lactamase among
   RT different species of Enterobacter, and filiation of the ACT-1
   RT plasmidic cephalosporinase to Enterobacter asburiae.";
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ416709; CAC95129.2; -.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.
FT NON_TER 373
FT SEQUENCE 373 AA; 40412 MW; C3C00BFD1335B305 CRC64;

O8VNT7 Length: 373 March 17, 2003 12:32 Type: P Check: 3072
Found using 'KTXS' (swope073.key)

...

285 MYGLGEMLMNPVDSKTIIDSDNKLALALPAREVNPAPPVKASVYHKTGSGFGS
335
345 YVAFIPKDLGITVMLANKSYNPAPVAYRRLSLAP
1--1
1 match found in sequence:
q8vypw1 ; Extended-spectrum beta-lactamase VEB-2.

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(from "lactxs_spt.pep")
TOIG of: q8vypw1 check: 5771 from: 1 to: 299

ID O8VPW1 PRELIMINARY; PRT; 299 AA.
AC O8VPW1;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Extended-spectrum beta-lactamase VEB-2.
GN BLAVER-2.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RA Gillich D., Naas T., Leelaopon A., Poirel L., Fennwald M.,
   Nordmann P.;
RT "Molecular epidemiology of extended spectrum VEB-1 containing
   RT Pseudomonas aeruginosa strains from Thailand.";
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY027870; AK29174.1; -.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; beta-lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
FT SEQUENCE 299 AA; 33705 MW; 24EA766F3CF4CC2F CRC64;

O8VPW1 Length: 299 March 17, 2003 12:32 Type: P Check: 5771
Found using 'KTXS' (swope073.key)

...

53 KDTLKINDFHFPQSYNKKEPIALAVSEIDKGNLSEQKIEITPPDLLPKTWSPIKEEF
103
113 PNGTTLTIEQLNTVSESDNIGCDILLKLTIGTDSYQKFLNAN
1--1
1 match found in sequence:
q8vq11 ; Extended-spectrum beta-lactamase CTX-M-5 (Fragment).
(from "lactxs_spt.pep")
TOIG of: q8vq11 check: 9928 from: 1 to: 276

ID O8VQ11 PRELIMINARY; PRT; 276 AA.
AC O8VQ11;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Extended-spectrum beta-lactamase CTX-M-5 (Fragment).
GN Acinetobacter baumannii.
OS Plasmid pSUN-5.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_Taxid=470;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUN-183;
RA Lu J., Tang Y.C., Wu B.Q., Zhang K.X., Zhu J.X., Tan S.Q., Bi X.G.;
RT "Plasmid-mediated extended-spectrum beta-lactamase CTX-M-5 in
   RT Acinetobacter Baumannii in China.";
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF462635; AAL68825.1; -.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; beta-lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
FT Plasmid.
FT NON_TER 1
FT SEQUENCE 1

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SQ SEQUENCE 276 AA; 29555 MW; 243E31A4C80977EA CRC64;
08VQ11 Length: 276 March 17, 2003 12:32 Type: P Check: 9928 ..
Found using 'KTXS' (swope073.key)

...

172 LAMAQTLNLTGKALAEFORADLVYTWKNTTGSASIRAGLPKSMGVGDGTGSGDYGT
222
232 NDIAVWPANHAPLVVTFYTPQEKAKESRSDVLAATAKIVTHG
...

1 match found in sequence:
q8vq12 : Extended-spectrum beta-lactamase CTX-M-3 (Fragment).
(from "lactxs_spt.pep")
TOIG of: q8vq12 check: 8396 from: 1 to: 253

ID 08VQ12 PRELIMINARY; PRT; 253 AA.
AC 08VQ12;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE Extended-spectrum beta-lactamase CTX-M-3 (Fragment).
OS Enterobacter cloacae.
OG Plasmid pSUN-4.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUN-178;
RA Lu J., Tang Y.C., Wu B.Q., Zhang K.X., Zhu J.X., Tan S.Q., Bi X.G.;
RT "Plasmid-mediated extended-spectrum beta-lactamase CTX-M-3 in
RT Enterobacter cloacae in China."
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF462634; AAL68824.1;
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase_1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
KW Plasmid.
FT NON_TER 1 1
FT NON_TER 253 253
SQ SEQUENCE 253 AA; 27114 MW; 8B9FCFE4B94B2CBD CRC64;

08VQ12 Length: 253 March 17, 2003 12:32 Type: P Check: 8396 ..
Found using 'KTXS' (swope073.key)

...

170 RAMAQTILNLTGKALGDSQAQLVTWMMKNTGASIAQGLPASWYVGDSGDYGT
1--1
220
230 NDIAVWPANHAPLVVTFYTPQEKAKESRSDVLAATAKIVTHG
...

1 match found in sequence:
q8vq75 : Late competence protein ComEC.
(from "lactxs_spt.pep")
TOIG of: q8vq75 check: 1307 from: 1 to: 795

ID 08VQ75 PRELIMINARY; PRT; 795 AA.
AC 08VQ75;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Late competence protein ComEC.

...

GN COMEC.
OC Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC14580;
RA Lapidus A., Galleron N., Andersen J.T., Jorgensen P.L., Ehrllich S.D.,
RA Sorokin A.;
RT "Co-linear scaffold of the Bacillus licheniformis and Bacillus
RT subtilis genomes and its use to compare their competence genes."
RL FEMS Microbiol. Lett. 0:0-0(2002).
DR EMBL: AF459916; AAL67526.1;
DR InterPro: IPR002106; AATRNA_ligaseII.
DR InterPro: IPR001279; Bactamase-like.
DR InterPro: IPR004477; COMEC_N-term.
DR InterPro: IPR004797; COMEC_Rec2.
DR Pfam: PF00753; lactamase_B_1.
DR TIGRFAMs: TIGR00360; COMEC_N-term; 1.
DR TIGRFAMs: TIGR00361; COMEC_Rec2; 1.
DR PROSITE: PS00179; AA-trna_ligase-II_1; UNKNOWN_1.
SQ SEQUENCE 795 AA; 87815 MW; D459C3FDD6270ABE CRC64;

08VQ75 Length: 795 March 17, 2003 12:32 Type: P Check: 1307 ..
Found using 'KTXS' (swope073.key)

...

384 LMNFFPIPIYFTIMPLSPGSLAIFCFHPLGEGAAAADRLVLWVSHQAVKTVASADV
434
444 FSAKPPDLLFFYFTAIFFLLLEKMSLRVMPISGLAAV
...

1 match found in sequence:
q8vtn0 : Beta-lactamase Huga.
(from "lactxs_spt.pep")
TOIG of: q8vtn0 check: 6032 from: 1 to: 298

ID 08VTN0 PRELIMINARY; PRT; 298 AA.
AC 08VTN0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-lactamase Huga.
GN HUGA.
OS Proteus penneri.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=102862;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21621310; PubMed=11751137;
RA Liasine N., Mader S., Ninet B., Metral C., Fouchereau-Peron M.,
RA Labia R., Auckenthaler R.;
RT "Postneurosurgical Meningitis Due to Proteus penneri with Selection of
RT a Ceftriaxone-Resistant Isolate: Analysis of Chromosomal Class A beta-
RT Lactamase Huga and Its LysR-Type Regulatory Protein HUGR."
RL Antimicrob. Agents Chemother. 46:216-219(2002).
DR EMBL: AF324468; AAL57765.1;
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase_1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
SQ SEQUENCE 298 AA; 32605 MW; B9EA244D171CF918 CRC64;

08VTN0 Length: 298 March 17, 2003 12:32 Type: P Check: 6032 ..
Found using 'KTXS' (swope073.key)

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...
187      IMAKSLALTLGDLGSGSQROQLVTWKGNTGDSIKAGLPKHMIVGDSGDYGT
      237      |---|
247      NDIAVIMPNHAPLILVYFTQGEKDAKRYKDIIMAKATEIYTKK
      ...
1 match found in sequence:
gbvvp3 : Extended-spectrum beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: gbvvp3 check: 8304 from: 1 to: 291
-----
ID      Q8VVP3      PRELIMINARY;      PRT;      291 AA.
AC      Q8VVP3;
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DE      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
OS      Kluysvera citrophila (Kluysvera cryocrescens).
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Kluysvera.
OX      NCBI_Taxid=580;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CIP 79.54;
RX      MEDLINE=21565754; PubMed=11709346;
RA      Decusser J.W., Poirel L., Nordmann P.;
RT      "Characterization of a Chromosomally Encoded Extended-Spectrum Class A
      beta-lactamase from Kluysvera cryocrescens.";
RL      Antimicrob. Agents Chemother. 45:3595-3598(2001).
DR      EMBL; AY026417; AAK08976.1; -.
DR      InterPro: IPR001466; Beta_lactamase.
DR      InterPro: IPR000871; Beta_lactamase_A.
DR      Pfam: PF00144; beta-lactamase; 1.
DR      PRINTS: PR00118; BLACTMASEA.
DR      PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
SQ      SEQUENCE 291 AA; 31013 MW; 09E927017E249CAA CRC64;

O8VVP3 Length: 291 March 17, 2003 12:32 Type: P Check: 8304 ..
Found using 'KTxs' (swope073.key)
...
187      RAMAQTLRNLTLGKALGDAQRAQLVTWKGNTGTASTIQAQLPASWVYGDKTSGSDYGT
      237      |---|
247      NDIAVIMPKDRAPLVLTFTYTPQPEAESRRDVLASAKIVTEG
      ...
1 match found in sequence:
gbx9g8 : Stalic acid transporter.
(from "lactxs_spt.pep")
TOIG of: gbx9g8 check: 8213 from: 1 to: 506
-----
ID      O8X9G8      PRELIMINARY;      PRT;      506 AA.
AC      O8X9G8;
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Stalic acid transporter.
GN      NANT OR 24582 OR ECS4097.
OS      Escherichia coli O157:H7.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Escherichia.
OX      NCBI_Taxid=83334;

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RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=0157:H7 / EDL933 / ATCC 700927;
RX      MEDLINE=21074935; PubMed=11206551;
RA      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA      Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA      Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA      Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamosis K.,
RA      Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA      Welch R.A., Blattner F.R.;
RT      "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL      Nature 409:529-533(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=0157:H7 / RMD 0509952;
RX      MEDLINE=21156231; PubMed=11258796;
RA      Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA      Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA      Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA      Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT      "Complete genome sequence of enterohaemorrhagic Escherichia coli
      O157:H7 and genomic comparison with a laboratory strain K-12.";
RL      DNA Res. 8:11-22(2001).
DR      EMBL; AE005550; AAG58352.1; -.
DR      EMBL; AP002564; BAB37520.1; -.
DR      InterPro: IPR000871; Beta_lactamase_A.
DR      InterPro: IPR004742; SA_transporter.
DR      InterPro: IPR003662; sub_transporter.
DR      Pfam: PF00083; sugar_tr; 1.
DR      TIGRFAMs: TIGR00891; 2A0112; 1.
DR      PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
KW      Complete proteome.
SQ      SEQUENCE 506 AA; 54704 MW; 1C2261455D7AA15 CRC64;

O8X9g8 Length: 506 March 17, 2003 12:32 Type: P Check: 8213 ..
Found using 'KTxs' (swope073.key)
...
453      TFWVILLIGLDMPSRVQWRMLRPEALRTHDAIDGKPPSGAVFGSARNDLVKTYS
      503      |---|
1 match found in sequence:
gbxs85 : Probable transmembrane protein.
(from "lactxs_spt.pep")
TOIG of: gbxs85 check: 4284 from: 1 to: 216
-----
ID      O8XS85      PRELIMINARY;      PRT;      216 AA.
AC      O8XS85;
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Probable transmembrane protein.
GN      RSP0596 OR RS03883.
OS      Ralstonia solanacearum (Pseudomonas solanacearum).
OC      Plasmid megaplasmid.
OC      Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC      Ralstonia.
OX      NCBI_Taxid=305;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=GM11000;
RX      MEDLINE=21681879; PubMed=11823852;
RA      Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA      Arlat M., Billault A., Brotlier P., Camus J.C., Cartolico L.,
RA      Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
RA      Gaspin C., Lave M., Moisan A., Robert C., Saurin W., Schlex T.,
RA      Stiguer P., Thebaud P., Boucher C.A.;
RT      "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL      Nature 415:497-502(2002).

```

DR EMBL: AL646079; CAD17747.1; -
 DR InterPro: IPR002106; AATRNA_ligaseII.
 DR InterPro: IPR001279; Blactmase-1like.
 DR Pfam: PF00753; lactamase_B.1.
 DR PROSITE: PS00339; AA_TPRNA_LIGASE_IL_2; UNKNOWN_1.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 216 AA; 23086 MW; 0DFB713803D4CAF5 CRC64;

08X85 Length: 216 March 17, 2003 12:32 Type: P Check: 4284
 Found using 'KTXS' (swope073.key)

...

150 AQLGVKPADHYVAISHTHPDHIGNVEMFPQAMLLVQKESPFGNSQMPAKTGSTTLRKP
 200

210 NSGIWPA

1 match found in sequence:
 q8y5b0 : Sepsa protein.
 (from "lactxs_spt.pep")

TOIG of: q8y5b0 check: 8668 from: 1 to: 633

ID Q8Y5B0 PRELIMINARY; PRT; 633 AA.
 AC Q8Y5B0;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Sepsa protein.
 GN SEPA OR LMO2157.
 OS Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 CC NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-E / SEROVAR 1/2A;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
 Chardit A., Chetouani F., Couve E., de Darvar A., Dehoux P.,
 Domain E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 Entlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft U., Kuhn M., Kunst F., Kurupat G.,
 Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
 RT "Comparative genomics of Listeria species."
 RL Science 294:849-852(2001).
 DR EMBL: AL591982; CAD00235.1; -
 DR Listlist; LMO02157; -
 DR InterPro: IPR001279; Blactmase-1like.
 DR InterPro: IPR001064; Crystallin.
 DR Pfam: PF00753; lactamase_B.1.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 633 AA; 71419 MW; 127950FB644B15B CRC64;

Q8Y5B0 Length: 633 March 17, 2003 12:32 Type: P Check: 8668
 Found using 'KTXS' (swope073.key)

...

174 KVALIGPEGNEAAVSENIFAGNMIRRAEYMGSRSLKRELQGVDAIGLKTASKGHMST
 224

234 LAPNDTTFDEHKRVVDGIEVEFLMAVNTAPSEHMYFPQFKL

1 match found in sequence:
 q8y740 : ComEC protein.
 (from "lactxs_spt.pep")

TOIG of: q8y740 check: 3695 from: 1 to: 740

ID Q8Y740 PRELIMINARY; PRT; 740 AA.
 AC Q8Y740;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ComEC protein.
 GN COMEC OR LMO1482.
 OS Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 CC NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-E / SEROVAR 1/2A;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
 Chardit A., Chetouani F., Couve E., de Darvar A., Dehoux P.,
 Domain E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 Entlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft U., Kuhn M., Kunst F., Kurupat G.,
 Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
 RT "Comparative genomics of Listeria species."
 RL Science 294:849-852(2001).
 DR EMBL: AL591979; CAC99560.1; -
 DR Listlist; LMO01482; -
 DR InterPro: IPR001279; Blactmase-1like.
 DR InterPro: IPR004477; COMEC_N-term.
 DR InterPro: IPR004797; COMEC_N-term.
 DR Pfam: PF00753; lactamase_B.1.
 DR TIGRPFMS: TIGR00360; COMEC_N-term; 1.
 DR TIGRPFMS: TIGR00361; COMEC_N-term; 1.
 KW Complete proteome.
 SQ SEQUENCE 740 AA; 83521 MW; A2DB394BA4D14197 CRC64;

Q8Y740 Length: 740 March 17, 2003 12:32 Type: P Check: 3695
 Found using 'KTXS' (swope073.key)

...

624 EGGNDSDIVLKAVALDDKWLFVGTGLEANGEMGISBPQIKADILKVGHHGSSSKKEFIQ
 674

684 KKKPTFAVISCGLNRRGHPHEETINTLETAGVTILRTDVGCEI

...

1 match found in sequence:
 q8y172 : Penicillin-binding protein 2.
 (from "lactxs_spt.pep")

TOIG of: q8y172 check: 6472 from: 1 to: 607

ID Q8Y172 PRELIMINARY; PRT; 607 AA.
 AC Q8Y172;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Penicillin-binding protein 2.
 GN BME10573.


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OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Møjer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jadhavskii L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letessier J.-J.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL: AE009499; AL51754.1; -.
DR InterPro: IPR000871; Beta_lactamase_A.
DR InterPro: IPR005311; PBP_dimer.
DR InterPro: IPR001460; Transpeptidase.
DR Pfam: PF03717; PBP_dimer: 1.
DR Pfam: PF00905; Transpeptidase: 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 607 AA; 66124 MW; 6776D54EF1859BC5 CRC64;

08Y172 Length: 607 March 17, 2003 12:32 Type: P Check: 6472 ..
Found using 'KTXS' (swope073.key)

...

57 AGIYVAGKLYFGMIGVDADGPFVHQLASRPDILDRNGEILATIDIKTASLAEPR 1--1
117 KIYDPDETIENTSTVLPDDWETATYRLKSGAGFWIKRGLTPK 107

1 match found in sequence:
q8ztd5 : mRNA 3'-end processing factor, conjectural.
(from "lactxs_spt.pep")
TOIG of: q8ztd5 check: 2403 from: 1 to: 430

ID 08ZTD5 PRELIMINARY; PRT; 430 AA.
AC 08ZTD5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE mRNA 3'-end processing factor, conjectural.
GN PAE3309.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL: AE009923; AL64827.1; -.
DR InterPro: IPR001279; Blactamase-like.
DR Pfam: PF00753; Lactamase_B; 1.
KW Complete proteome.
SQ SEQUENCE 430 AA; 47570 MW; 4147D753E1021A02 CRC64;

08ZTD5 Length: 430 March 17, 2003 12:32 Type: P Check: 2403 ..
Found using 'KTXS' (swope073.key)

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1 MKRIILGAGEVGRALAVIKRTASNGILIDYGVSPDANKPVFPFLAVRPDLTATFLSHAH 1--1
20 23
61 LDHSGGLPSLYVS

...

1 match found in sequence:
q8ztd9 : mRNA 3'-end processing factor, conjectural.
(from "lactxs_spt.pep")
TOIG of: q8ztd9 check: 1997 from: 1 to: 634

ID 08ZTD9 PRELIMINARY; PRT; 634 AA.
AC 08ZTD9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE mRNA 3'-end processing factor, conjectural.
GN PAE0820.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL: AE009787; AL63054.1; -.
DR InterPro: IPR001279; Blactamase-like.
DR Pfam: PF00753; Lactamase_B; 1.
KW Complete proteome.
SQ SEQUENCE 634 AA; 71173 MW; 744B1B475DD56D24 CRC64;

08ZTD9 Length: 634 March 17, 2003 12:32 Type: P Check: 1997 ..
Found using 'KTXS' (swope073.key)

...

18 EIVKVNVEGPNLCIYKRPTEVDIMIGEVAKTLKRYILRVDPNSNRASEXTASKVIREV 1--1
68 71
78 LSDVEDVVFENNGVDYIYLAFLAKREKIKSXTRELFVKTGMRAV

...

1 match found in sequence:
q92cz5 : Hypothetical protein lmo1027.
(from "lactxs_spt.pep")
TOIG of: q92cz5 check: 7696 from: 1 to: 555

ID 092CZ5 PRELIMINARY; PRT; 555 AA.
AC 092CZ5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein lmo1027.
GN LMO1027 OR LMO1026.
OS Listeria monocytogenes, and
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639, 1642;
RN [1]

```

RP SEQUENCE FROM N.A.
RC SPECIES=L.monocytogenes, and L.innocua;
RC STRAIN=EGC-E / SEROVAR 1/2A, AND CLIP 11262 / SEROVAR 6A.
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Blocher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Darivar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kunz M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mala Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RT "Comparative genomics of *Listeria* species.",
RL Science 294:849-852(2001).
DR EMBL: AL591977; CAC99105.1; -
DR EMBL: AL596167; CAC96257.1; -
DR Listlist: LINO1026; -
DR Listlist: LMO01027; -
DR InterPro: IPR001279; Blactmase-like.
DR InterPro: IPR004613; MG423.
DR InterPro: IPR001587; UPE0036.
DR Pfam: PF00753; Lactamase-B; 1.
DR Pfam: PF02147; UPE0036; 1.
DR TIGRFAMS: TIGR00649; MG423; 1.
DR PROSITE: PS01292; UPE0036; UNKNOWN.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 555 AA; 61559 MW; 990B7F9A186FF59E CRC64;

Q92C25 Length: 555 March 17, 2003 12:32 Type: P Check: 7696
Found using 'KTXS' (swope073.key)

103 LIRNLEEHGLRQKTYEEDVFKFRKTSISFRTTHSIPPTYGIVVTPSGNIVHT
153
163 GDFKFDTPVGEPAHLTKMAEIGKEGVCLLSDSTNAEVPNFTM

1 match found in sequence:
q92g80 ; Similarity to beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q92g80 check: 7816 from: 1 to: 100

ID Q92G80 PRELIMINARY; PRT; 100 AA.
AC Q92G80;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Similarity to beta-lactamase.
GN RCI243.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiase; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Reneato-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenhach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in *Rickettsia conorii* and *R. prowazekii*.",
RL Science 293:2093-2098(2001).
DR EMBL: AE008671; AAL03781.1; -
KW Complete proteome.
SQ SEQUENCE 100 AA; 11819 MW; E2CE1715E308E150 CRC64;

Q92G80 Length: 100 March 17, 2003 12:32 Type: P Check: 7816
Found using 'KTXS' (swope073.key)

1 MPVSQAQEMTKNLFIEFDVDCMKRYGKSGCNKLSODRTYKLDKRRKIGWFGWLQKND
29 32
61 RTVEFVHFIEENKNKYDSYAGOR

1 match found in sequence:
q92uq4 ; Putative exported beta-lactamase protein (EC 3.5.2.6).
(from "lactxs_spt.pep")
TOIG of: q92uq4 check: 1703 from: 1 to: 396

ID Q92UQ4 PRELIMINARY; PRT; 396 AA.
AC Q92UQ4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative exported beta-lactamase protein (EC 3.5.2.6).
GN AMPC OR RB1040 OR SM21600.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid PSYMB (megaplasmid 2).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhmester J., Chain P.,
RA Vorhoefer F.U., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont *Sinorhizobium meliloti*.",
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR EMBL: AL603645; CAC49440.1; -
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase-C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE-C; UNKNOWN.1.
KW Hydrolyase; Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 396 AA; 42667 MW; 5E8FB5B3ECE24692 CRC64;

Q92UQ4 Length: 396 March 17, 2003 12:32 Type: P Check: 1703
Found using 'KTXS' (swope073.key)

291 MTOGLGWEVYPTTKLDDLGNSSRMALPDKVSKLVPAPQENLWINKGSGTNGFCA
341
351 YAAVPAERIGIVMLANRNPPIPARVKAAYQILSTLSEGPSAD

1 match found in sequence:
q933m6 ; Beta-lactamase AmpC precursor (EC 3.5.2.6).
(from "lactxs_spt.pep")
TOIG of: q933m6 check: 1351 from: 1 to: 381

ID Q933M6 PRELIMINARY; PRT; 381 AA.
AC Q933M6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Beta-lactamase AmpC precursor (EC 3.5.2.6).

GN AMPC.
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K99230, AND K9914325;
 RA Lee S.H., Jeong S.H., Lee K.J.;
 RT "Complete sequence of AmpC beta-lactamase gene."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF411146; AL05855.1; -
 DR EMBL; AF411147; AL05856.1; -
 DR EMBL; AF411149; AL05858.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase_1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 20 . POTENTIAL.
 FT CHAIN 21 381 BETA-LACTAMASE AMPC.
 SQ SEQUENCE 381 AA; 41251 MW; 67912CBF5CB03C93 CRC64;
 O93M6 Length: 381 March 17, 2003 12:32 Type: P Check: 1351 ..
 Found using 'KTxs' (swope073.key)

285 MYGIGEMLMNPVANTVVEGSDSKVALAPVAEVNPPAPPYKASWVHTGTGSGFGS
 335
 345 YVAFIPEKIGIVMLANKSYNPARVEAAYHILEALQ

1 match found in sequence:
 q93jr1; Beta-lactamase AmpC precursor (EC 3.5.2.6).
 (from "lactxs_spt.pep")
 TOIG of: q93jr1 check: 1305 from: 1 to: 381
 ID O93JR1 PRELIMINARY; PRT; 381 AA.
 AC O93JR1.
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Beta-lactamase AmpC precursor (EC 3.5.2.6).
 GN AMPC.
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K992004.1, AND K995120.1;
 RA Lee S.H., Jeong S.H., Lee K.J.;
 RT "Complete sequence of AmpC beta-lactamase gene."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF411144; AL05853.1; -
 DR EMBL; AF411145; AL05854.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase_1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 20 . POTENTIAL.
 FT CHAIN 21 381 BETA-LACTAMASE AMPC.
 SQ SEQUENCE 381 AA; 41271 MW; 50013EBB8B75C2F CRC64;
 O93JR1 Length: 381 March 17, 2003 12:32 Type: P Check: 1305 ..
 Found using 'KTxs' (swope073.key)

285 MYGIGEMLMNPVANTVVEGSDSKVALAPVAEVNPPAPPYKASWVHTGTGSGFGS
 335

345 YVAFIPEKIGIVMLANKSYNPARVEAAYHILEALQ

1 match found in sequence:
 q936v5; CTX-M-2 like beta-lactamase.
 (from "lactxs_spt.pep")
 TOIG of: q936v5 check: 7709 from: 1 to: 291
 ID O936V5 PRELIMINARY; PRT; 291 AA.
 AC O936V5.
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE CTX-M-2 like beta-lactamase.
 GN BLACTX-M-2 LIKE.
 OS Proteus mirabilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Proteus.
 OX NCBI_TaxID=584;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TLR;
 RA Saladin M., Bao Cao V.T., Lambert T., Donay J.L., Herrmann J.L.,
 Ould Hocine Z., Verdet C., Delisle F., Philippin A., Arlet G.;
 RT "Diversity of CTX-M beta-lactamases and their promoter regions from
 enterobacteriaceae isolated in three hospitals of downtown Paris."
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ146344; CAC95175.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase_1.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
 SQ SEQUENCE 291 AA; 31412 MW; 82277CD9C1B2E7C0 CRC64;
 O936V5 Length: 291 March 17, 2003 12:32 Type: P Check: 7709 ..
 Found using 'KTxs' (swope073.key)

187 LMAQITLKNLTGKALAEYORADLVYWKGNNTGSASIRAGLPKSVVGDGTGSGYTT
 237

247 NDIAVIVPENHAPLVIVTYFTPEOKAESRDFLAATAKIVTHG

1 match found in sequence:
 q937j1; CTX-M-9 like beta-lactamase.
 (from "lactxs_spt.pep")
 TOIG of: q937j1 check: 8277 from: 1 to: 291
 ID O937J1 PRELIMINARY; PRT; 291 AA.
 AC O937J1.
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE CTX-M-9 like beta-lactamase.
 GN BLACTX-M-9 LIKE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TRA;
 RA Saladin M., Bao Cao V.T., Lambert T., Donay J.L., Herrmann J.L.,
 Ould Hocine Z., Verdet C., Delisle F., Philippin A., Arlet G.;

RT "Diversity of CTX-M beta-lactamases and their promoter regions from
 RT enterobacteriaceae isolated in three hospitals of downtown Paris."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A416346; CAD08929.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
 DR SEQUENCE 291 AA; 30897 MW; 528D4DA306A06606 CRC64;
 SQ

Q937J1 Length: 291 March 17, 2003 12:32 Type: P Check: 8277 ..
 Found using 'KTXS' (swope073.key)

187 RAMAQTLLRLTGLHGETGORAQVLTWLGKNTTGAASIRAGLPTSWTGDKSGSDGYTT
 237

247 NDIAVIMPGRAPLVLTFTPTQPONAESRRDVLASARIIAEG

2 matches found in sequence:
 q937t8 : Class C beta-lactamase.
 (from "lactxs_spt.pep")

TOIG of: q937t8 check: 1722 from: 1 to: 383

ID Q937t8 PRELIMINARY; PRT; 383 AA.
 AC Q937t8;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Class C beta-lactamase.
 GN AMPC.
 OS Butiauxella sp. BTN01.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Butiauxella.
 OX NCBI_TaxID=173478;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BTN01;
 RA Fihman V., Delisle F., Benzerara L., Nadjar D., Labia R.,
 RA Philippot A., Arlet G.;
 RT "BT-1: a new member of the inducible class C beta-lactamases club
 RT from a clinical isolate of the genus Butiauxella."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ415568; CAC94553.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN_1.
 DR SEQUENCE 383 AA; 41779 MW; BEBF49C23E0DA740 CRC64;
 SQ

Q937t8 Length: 383 March 17, 2003 12:32 Type: P Check: 1722 ..
 Found using 'KTXS' (swope073.key)

1 MMKKTLOCALVLSASFAPAAOKTISDKQEDVDVNTLKPMITAOAIPGMAVAIVYQKP
 23 26

61 HYFTYGVADIAROPV

...

287 MYOGLGEMNLMPVAAATVINGSDNKVYALASPVTALEPPVAFKASLVHKIGSTNGFCA
 337

347 YVAFIPKQIGIYVLANKMYPTNERVAKANTLLNTIQ

1 match found in sequence:
 q939k2 : Beta-lactamase CTX-M-16.
 (from "lactxs_spt.pep")
 TOIG of: q939k2 check: 8726 from: 1 to: 291

ID Q939k2 PRELIMINARY; PRT; 291 AA.
 AC Q939k2;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Beta-lactamase CTX-M-16.
 GN BLACTX-M-16.
 OS Klebsiella pneumoniae.
 OG Plasmid pIP843.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BM4493;
 RA Cao V.T.B., Lambert T., Courvalin P.;
 RT "Characterization of COL1-like plasmid encoding the cefotaxime-
 RT hydrolyzing beta-lactamase CTX-M-16 (blactX-M-16) gene."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY033516; AAK71471.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
 DR Plasmid.
 KW SEQUENCE 291 AA; 30978 MW; C8DC15572EAE465E CRC64;
 SQ

Q939k2 Length: 291 March 17, 2003 12:32 Type: P Check: 8726 ..
 Found using 'KTXS' (swope073.key)

187 RAMAQTLLRLTGLHGETGORAQVLTWLGKNTTGAASIRAGLPTSWTGDKSGSDGYTT
 237

247 NDIAVIMPGRAPLVLTFTPTQPONAESRRDVLASARIIAKG

1 match found in sequence:
 q939d4 : Beta-lactamase CTX-M-16.
 (from "lactxs_spt.pep")

TOIG of: q939d4 check: 8618 from: 1 to: 291

ID Q939d4 PRELIMINARY; PRT; 291 AA.
 AC Q939d4;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Beta-lactamase CTX-M-16.
 GN Escherichia coli.
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21344617; PubMed=11451684;
 RA Bonnet R., Dutour C., Sampaio J.L., Chanal C., Siroi D., Labia R.,
 RA De Champs C., Siroi J.;
 RT "Novel cefotaxime (CTX-M-16) with increased catalytic efficiency due
 RT to substitution Asp-240->Gly."
 RL Antimicrob. Agents Chemother. 45:2269-2275(2001).
 DR EMBL: AY029068; AAK32961.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.

DR PROSITE; PS00146; BETA-LACTAMASE_A; UNKNOWN_1.
 SQ SEQUENCE 291 AA; 30893 MW; C8C9411A8D29469E CRC64;
 0939N4 Length: 291 March 17, 2003 12:32 Type: P Check: 8618
 Found using 'KTXS' (swope073.key)

187 RAMAQTRLQTLTGALGETORQALVTWLGKNTTGASIRAGLPTSWTADKGTSGSGYGT
 237

247 NDIAVIMPOGRAPLVLYTYFTQPOQNAESRDVLAASARIIEG

1 match found in sequence:
 q93ca2 ; Beta-lactamase AmpC precursor (EC 3.5.2.6).
 (from "lactxs_spt.pep")
 TOIG of: q93ca2 check: 2682 from: 1 to: 381

ID 093CA2 PRELIMINARY; PRT; 381 AA.
 AC 093CA2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-lactamase Ampc precursor (EC 3.5.2.6).
 GN AMPC.
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K9973;
 RA Lee S.H., Jeong S.H., Lee K.J.;
 RT "Complete sequence of Ampc beta-lactamase gene."
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF411148; AAL05857.1;
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase.
 DR Pfam; PF00144; beta_lactamase_1.
 DR PROSITE; PS00336; BETA-LACTAMASE_C; UNKNOWN_1.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 381 BETA-LACTAMASE AMPC.
 SQ SEQUENCE 381 AA; 41341 MW; 31A3C4659A361921 CRC64;
 093CA2 Length: 381 March 17, 2003 12:32 Type: P Check: 2682
 Found using 'KTXS' (swope073.key)

285 MTCGLGEMLMKPVYANTVVEGSDSKVALADLPVYVNPAPYKASVNHGTGSGFGFS
 335

345 YVAFIPKQIGIVMLANTSYNPARVEAAVHLEALQ

1 match found in sequence:
 q93et5 ; Class A beta-lactamase.
 (from "lactxs_spt.pep")
 TOIG of: q93et5 check: 4701 from: 1 to: 295

ID 093ET5 PRELIMINARY; PRT; 295 AA.
 AC 093ET5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Class A beta-lactamase.
 GN BLARAHN-1.

OS Rahnelia aquatilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Rahnelia.
 OX NCBI_TaxID=34038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21441186; PubMed=11557504;
 RA Bellais S., Poirel L., Fortineau N., Decusser J.W., Nordmann P.;
 RT "Biochemical-Genetic Characterization of the Chromosomally Encoded
 Extended-Spectrum Class A beta-lactamase from Rahnelia aquatilis."
 RL Antimicrob. Agents Chemother. 45:2965-2968(2001).
 DR EMBL; AF338038; AAK83220.1;
 DR InterPro: IPR001466; Beta_lactamase.
 DR Pfam; PF00144; beta_lactamase_1.
 SQ SEQUENCE 295 AA; 31892 MW; 137459B7B84C18EB CRC64;

093ET5 Length: 295 March 17, 2003 12:32 Type: P Check: 4701
 Found using 'KTXS' (swope073.key)

191 RAMALSIQHTATGSLALPORQALVEMWKNTTGAMSIKAGLPTATWYVGDKGTSGSGYGT
 241

251 NDIAVIMPENKAPLVLYTYFTQPEKDAKSRDVLASAKIYVTC

1 match found in sequence:
 q93f82 ; Ceftazidime-hydrolyzing beta-lactamase CTX-M-19.
 (from "lactxs_spt.pep")
 TOIG of: q93f82 check: 8870 from: 1 to: 291

ID 093F82 PRELIMINARY; PRT; 291 AA.
 AC 093F82;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Ceftazidime-hydrolyzing beta-lactamase CTX-M-19.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Poirel L., Naas T., Le Thomas L., Karim A., Bingen E., Nordmann P.;
 RT "CTX-M-type extended-spectrum beta-lactamase that hydrolyzes
 ceftazidime through a single amino acid substitution in the omega
 loop."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF325134; AAK55534.1;
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; beta_lactamase_1.
 DR PROSITE; PS00146; BETA-LACTAMASE_A; UNKNOWN_1.
 SQ SEQUENCE 291 AA; 30969 MW; C8DDCD742EAE469D CRC64;

093F82 Length: 291 March 17, 2003 12:32 Type: P Check: 8870
 Found using 'KTXS' (swope073.key)

187 RAMAQTRLQTLTGALGETORQALVTWLGKNTTGASIRAGLPTSWTADKGTSGSGYGT
 237

247 NDIAVIMPOGRAPLVLYTYFTQPOQNAESRDVLAASARIIEG

1 match found in sequence:
 q93n98 : AmpC.
 (from "lactxs_spt.pep")
 TOIG of: q93n98 check: 4213 from: 1 to: 378

.....

ID Q93N98 PRELIMINARY; PRT; 378 AA.
 AC Q93N98;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE AmpC.
 GN AmpC.
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 OX NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1;
 RA Mahlen S.D., Morrow S.S., Hanson N.D.;
 RT "Sequence and transcriptional analysis of the ampC gene of Serratia
 marcescens reveals unique regulatory properties."
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF384203; AAK6454.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR Pfam: PF00144; beta_lactamase_C.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; UNKNOWN.1.
 SQ SEQUENCE 378 AA; 41262 MW; 45246C83A5683D33 CRC64;

Q93N98 Length: 378 March 17, 2003 12:32 Type: P Check: 4213 ..
 Found using 'KTXS' (swope073.key)

.....

280 FTQDLMMENPYPKLSRLTEGNNAGIMNGTPATITTPPELRAAGWYKGTSGGFST
 330

340 YAVFPAKNAIVMLANKFPPNDREVAHYHYVALEKR

.....

1 match found in sequence:
 q93rk2 : Penicillin-binding protein 4 (Fragment).
 (from "lactxs_spt.pep")
 TOIG of: q93rk2 check: 2729 from: 1 to: 424

.....

ID Q93RK2 PRELIMINARY; PRT; 424 AA.
 AC Q93RK2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Penicillin-binding protein 4 (Fragment).
 GN DABC.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MT196;
 RA Ubukata K., Shibasaki Y., Yamamoto K., Chiba N., Hasegawa K.,
 RA Takeuchi Y., Sunakawa K., Inoue M., Kono M.;
 RT "Association of amino acid substitutions in penicillin-binding protein
 3 with beta-lactam resistance in beta-lactamase-negative Ampicillin-
 resistant Haemophilus influenzae."
 RT Antimicrob. Agents Chemother. 0:0-0(2001).
 RL EMBL: AB035864; BAB58902.1; -
 DR InterPro: IPR000667; Peptidase_S13.
 DR Pfam: PF02113; Peptidase_S13; I.
 DR TIGRFAMs: TIGR00666; PPP4; I.
 FT NON_TER 1 1
 FT NON_TER 424 424

SQ SEQUENCE 424 AA; 46368 MW; 050F80ADB03BFDD0 CRC64;
 Q93RK2 Length: 424 March 17, 2003 12:32 Type: P Check: 2729 ..
 Found using 'KTXS' (swope073.key)

.....

344 PKTMLSVLEIYAKNEDKHLMETPEPIAGVDTISGRGLISPLVKNVIAKTSGLKGVN
 394

404 LAGFMTNAGEKVAFFVQFING

.....

1 match found in sequence:
 q93spt1 : Methyl parathion degrading protein.
 (from "lactxs_spt.pep")
 TOIG of: q93spt1 check: 1637 from: 1 to: 341

.....

ID Q93SPT1 PRELIMINARY; PRT; 341 AA.
 AC Q93SPT1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Methyl parathion degrading protein.
 OS Plesiomonas sp. DDL-1.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Plesiomonas.
 OX NCBI_TaxID=158201;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DL-1;
 RA Liu Z., Li S.P.;
 RT "Cloning and expression of MP (methyl parathion) degrading gene (DMP)
 from Plesiomonas sp.";
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AY029773; AAK40367.1; -
 DR InterPro: IPR001969; Asparticase_site.
 DR InterPro: IPR001279; Blactamase-like.
 DR Pfam: PF00753; lactamase_B; I.
 DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN.1.
 SQ SEQUENCE 341 AA; 36073 MW; ABC9B8C4D4CDB56 CRC64;

Q93SPT1 Length: 341 March 17, 2003 12:32 Type: P Check: 1637 ..
 Found using 'KTXS' (swope073.key)

.....

39 LVSTAHAAPEVETSAAGYYRMLGDDEITLSDGTVALPVDKRLNQPAKTSALAKSF
 89 92

99 QKAPLETSTGYLVNNGSKLVLDVGAGAGLFGPTLGRLANLKA

.....

1 match found in sequence:
 q95qv2 : Hypothetical 142.4 kDa protein.
 (from "lactxs_spt.pep")
 TOIG of: q95qv2 check: 6781 from: 1 to: 1247

.....

ID Q95QV2 PRELIMINARY; PRT; 1247 AA.
 AC Q95QV2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 142.4 kDa protein.
 GN C18C4.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Gattung S.;
RT "The sequence of C. elegans cosmid C18C4.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U53369; AAK52175.1; -.
DR InterPro: IPR001140; ABCtransportrTM.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00664; ABC_membrane_1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
DR Hypothetical protein.
KW SEQUENCE 1247 AA; 142354 MW; BF848462AB0C4B16 CRC64;

Q95QV2 Length: 1247 March 17, 2003 12:32 Type: P Check: 6781
Found using 'KTXS' (swope073.key)
...
254 LKQOLKCRDERVEFEKTVLNSMTIKMFSEPHFKKLSMGKELSVRKRLSLNSFMH
      |---|
      304
314 SLNWTSPVITFEVFAVYGLQYELISALREFDAFVLIAIFNMR
      |---|
      304
1 match found in sequence:
q966b8 ; Hypothetical protein Y46H3D.6.
(from "lacktxs_spt.pep")
FOIG of: q966b8 check: 7338 from: 1 to: 345
-----
ID Q966B8 PRELIMINARY; PRT; 345 AA.
AC Q966B8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Hypothetical protein Y46H3D.6.
GN Y46H3D.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Stoneking T.; Wohlmann P.; Lennox S.;
RT "The sequence of C. elegans cosmid Y46H3D.";

```

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RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; AC006777; AAK72309.1; -.
DR InterPro: IPR000871; Beta_lactamase_A.
DR InterPro: IPR000536; Hormone_rec_1fg.
DR InterPro: IPR001628; znf_casteroid.
DR Pfam: PF00105; hormone_rec_1.
DR Pfam: PF00105; znf_C4; 1.
DR PRODOM: PD000035; znf_Casteroid; 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
  Zinc-finger.
KW SEQUENCE 345 AA; 39409 MW; 296817FB0FDB9B13 CRC64;

Q966B8 Length: 345 March 17, 2003 12:32 Type: P Check: 7338
Found using 'KTXS' (swope073.key)
...
291 TAGDYSLRAVEYVYLLQSVOKSLAIMHCKTLGYFDFDRFTCPINDNLETHSK
      |---|
      341
1 match found in sequence:
q97fa2 ; Predicted nucleotide-binding protein, yjeE family.
(from "lacktxs_spt.pep")
FOIG of: q97fa2 check: 7129 from: 1 to: 152
-----
ID Q97FA2 PRELIMINARY; PRT; 152 AA.
AC Q97FA2;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Predicted nucleotide-binding protein, yjeE family.
GN CAC2838.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J.; Breton G.; Omelchenko M.V.; Makarova K.S.; Zeng Q.;
RA Gibson R.; Lee H.W.; Dubois J.; Qiu D.; Hilti J.; Wolf Y.I.;
RA Tatusov R.L.; Sabathe F.; Doucette-Stamm L.; Soucaille P.; Daly M.J.;
RT "Genome sequence and comparative analysis of the solvent-producing
  bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007781; AAK80782.1; -.
DR InterPro: IPR000871; Beta_lactamase_A.
DR InterPro: IPR003442; UPF0079.
DR Pfam: PF02367; UPF0079; 1.
DR TIGRfams: TIGR00150; UPF0079; 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
KW Complete proteome.
KW SEQUENCE 152 AA; 17248 MW; 063955AB356C3ED3 CRC64;

Q97FA2 Length: 152 March 17, 2003 12:32 Type: P Check: 7129
Found using 'KTXS' (swope073.key)
...
1 MEFIVDSVKTFTSIGEOGLALAMPGDIVICINGDLGAKGTHFTWGIANKGNIETYITSPTF
      |---|

```

10 13

61 NIV

1 match found in sequence:
 q98ka7 ; Penicillin-binding protein.
 (from "lacks-spt.pep")

TOIG of: q98ka7 check: 4549 from: 1 to: 569

 ID O98ka7 PRELIMINARY; PRT; 569 AA.
 AC O98ka7;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Penicillin-binding protein.
 GN M11561.
 OS Rhizobium loti (Mesorhizobium loti)
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti."
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP002997; BAB48907.1;
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR InterPro: IPR005311; PBP_dimer.
 DR InterPro: IPR001460; Transpeptidase.
 DR Pfam: PF03717; PBP_dimer; 1.
 DR Pfam: PF00905; Transpeptidase; 1.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 569 AA; 61997 MW; 99FE82549E0AED48 CRC64;
 O98ka7 Length: 569 March 17, 2003 12:32 Type: P Check: 4549 ..
 Found using 'KTXS' (swope073.key)

 41 VFFGFTISGRIVYLGFGTPTDLSGGQSRITASRPDIYDRNGEVLTADIKTASLFAEPR
 1--1
 91 94
 101 RIVDADEAIERKSTVLPEDIDYEQTYHKLKSGAGFVWTLQRLTPK

 1 match found in sequence:
 q98lr0 ; Hypothetical protein m110916.
 (from "lacks-spt.pep")
 TOIG of: q98lr0 check: 5108 from: 1 to: 250

 ID O98lr0 PRELIMINARY; PRT; 250 AA.
 AC O98lr0;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein m110916.
 GN M110916.
 OS Rhizobium loti (Mesorhizobium loti)
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti."
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP002996; BAB48403.1;
 DR InterPro: IPR002137; Beta_lactamase_D.
 DR PROSITE: PS00337; BETA_LACTAMASE_D; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 250 AA; 27413 MW; DE134E74A46CF47E CRC64;

O98lr0 Length: 250 March 17, 2003 12:32 Type: P Check: 5108 ..
 Found using 'KTXS' (swope073.key)

 134 VNSLKITPVEQVDFLRKLARKLPVSAKAYDLTSATIPFQAGGWFVQKGTSTRLADD
 1--1
 184

194 ADKISDRSLGWFVGAKKDGQIVFARLVDTATDMPKGLKT

 1 match found in sequence:
 q98pl8 ; Hypothetical protein MYPV_7040.
 (from "lacks-spt.pep")
 TOIG of: q98pl8 check: 5305 from: 1 to: 631

 ID O98pl8 PRELIMINARY; PRT; 631 AA.
 AC O98pl8;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein MYPV_7040.
 GN MYPV_7040.
 OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-UAB CT1P;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chandaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Moszer I., Dydvig K., Wroblewski H., Viat I., Rocha E.P.C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 Mycoplasma pulmonis."
 RL Nucleic Acids Res. 29:2145-2153(2001).
 DR EMBL: AL445565; CAC13877.1;
 DR Mypulist; MYPV_7040;
 DR InterPro: IPR001279; Blactamase_1like.
 DR InterPro: IPR002029; Pepsidase_S8.
 DR InterPro: IPR001587; UPE0036.
 DR Pfam: PF00753; lactamase_B; 1.
 DR Pfam: PF02147; UPR0036; 1.
 DR PROSITE: PS00136; SUBTYLASE_ASP; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 631 AA; 71304 MW; 096B3AB60AE6A08A CRC64;
 O98pl8 Length: 631 March 17, 2003 12:32 Type: P Check: 5305 ..
 Found using 'KTXS' (swope073.key)


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...
564 AFNVKNNVNSKSKKKTLKSKNKSILEKYKQIFDDQDNKAKKSKTKSTKEPK
      614
624 EDDYDNI
-----
1 match found in sequence:
q99mz6 ; Myosin-VIIB.
(from "lactxs_spt.pep")
ToIG of: q99mz6 check: 1178 from: 1 to: 2113
ID Q99M26 PRELIMINARY; PRT; 2113 AA.
AC Q99M26
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myosin-VIIB.
GN MYO7B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21295050; PubMed=11401444;
RA Chen Z.-Y., Hasson T., Zhang D.-S., Schwender B.J., Derfler B.H.,
RA Mosseker M.S., Corey D.P.;
RT "Myosin VIIB, a novel unconventional myosin, is a constituent of
RT microvilli in transporting epithelia."
RT Genomics 72:285-296(2001).
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: AF242411; AAK28339.1; -.
DR HSSP: P08799; 1AMD.
DR MGD: MGI:107709; Myo7b.
DR InterPro: IPR002106; AATRNA_ligaseII.
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000871; Beta_lactamase_A.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR000857; MYTH4.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR000508; SigPase.
DR Pfam: PF00612; IQ_5.
DR Pfam: PF00063; myosin_head_1.
DR Pfam: PF00784; MYTH4_2.
DR PRINTS: PR00018; SH3_1.
DR PRODOM: PD000355; myosin_head_1.
DR SMART: SM00295; B41_2.
DR SMART: SM00015; IQ_4.
DR SMART: SM00242; MYSC_1.
DR SMART: SM00139; MYTH4_2.
DR SMART: SM00326; SH3_1.
DR PROSITE: PS00339; AA-TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS50057; BAND_41_3; 2.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
DR PROSITE: PS50002; SH3_1.
DR PROSITE: PS00761; SPASE_1_3; UNKNOWN_1.
DR SH3 domain.
SQ SEQUENCE 2113 AA; 240785 MW; FCB809163D0DC869 CRC64;

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Q99M26 Length: 2113 March 17, 2003 12:32 Type: P Check: 1178
 Found using 'KTXS' (swope073.key)

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1070 EFAFEDGPISDRPMNSLEKHFIVGTAIMRGLDELYCOICKQLSENKTSRAGWI
      1120

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1130 LLSLCGCFPPSERFMKYLINFISQGPSPSYGPPCAERLQRTFAN

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...
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2 matches found in sequence:
q99px9 ; Extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
(from "lactxs_spt.pep")
ToIG of: q99px9 check: 35 from: 1 to: 382

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ID Q99PX9 PRELIMINARY; PRT; 382 AA.
AC Q99PX9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN BLAQM-11.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K98678.3; AND K983802.1;
RA Lee S.H., Jeong S.H., Lee K.J.;
RT "Complete sequence of a novel bla(CMY-11) gene."
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF357599; AAK31370.1; -.
DR EMBL: AF357600; AAK31371.1; -.
DR EMBL: AF381619; AAK59973.1; -.
DR EMBL: AF381620; AAK59974.1; -.
DR EMBL: AF381621; AAK59975.1; -.
DR EMBL: AF381622; AAK59976.1; -.
DR EMBL: AF381623; AAK59977.1; -.
DR EMBL: AF381624; AAK59978.1; -.
DR EMBL: AF381625; AAK59979.1; -.
DR EMBL: AF381626; AAK59980.1; -.
DR HSSP: P05364; 2BLF.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta_lactamase_1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
DR KMW SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 382 AA; 40798 MW; F9006A5ED535812E CRC64;

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Q99PX9 Length: 382 March 17, 2003 12:32 Type: P Check: 35
 Found using 'KTXS' (swope073.key)

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199 EQLTLPLGLMHHHTYVNPVKQAMASVAYGSKEDKPIRVNGLADRAVYGIKISSADLLRP
      249

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259 VKANIGGVDDKALQQAISLTHGHGYSVGWTOGLGWESYAYPYTEQTLLAGNSAKVSLAE
      335
319 NPTAAPREGSGYLVNKTGSTNGFGAIVAFVAPARGIGIYMLANRNPIDARIKAAHAIIIA

```

379 QLAG

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2 matches found in sequence:
q99gcl ; Extended-spectrum beta-lactamase precursor (EC 3.5.2.6).

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(from "lactxs_spt.pep")
TOIG of: q99qcl check: 9735 from: 1 to: 382
ID 099QCL PRELIMINARY; PRT; 382 AA.
AC 099QCL;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN BLACMW-10.
OS Enterobacter aerogenes (Aerobacter aerogenes),
OS Escherichia coli, and
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=548, 562, 573;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.aerogenes; STRAIN=K995747.1, AND K9911729;
RA Lee S.H., Jeong S.H., Lee K.J.;
RT "Complete sequence of a novel bla(CMW-10) gene."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli, and K.pneumoniae;
RC STRAIN=K99B3053, K997048, K998298, AND K99B3386;
RA Lee S.H., Jeong S.H., Lee K.J.;
RT "Complete sequence of a novel bla(CMW-10) gene."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF37597; AAK31368.1; -
DR EMBL; AF37598; AAK31369.1; -
DR EMBL; AF381615; AAK59969.1; -
DR EMBL; AF381616; AAK59970.1; -
DR EMBL; AF381617; AAK59971.1; -
DR EMBL; AF381618; AAK59972.1; -
DR HSSP; P03364; 2BT.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW Hydrolase; Signal.
FT SIGNAL 1
SQ SEQUENCE 382 AA; 40824 MW; 7B06A4B20D594DB CRC64;
...
099QCL Length: 382 March 17, 2003 12:32 Type: P Check: 9735
Found using 'KTXS' (swope073.key)
...
199 EOTLLPGIGMHTYVNVPKQAMASYAYGSKDKPIHVNPGLADEAYGIGKTSADLLRF 1--|
249
259 VKANIGVDKDALQQAISLTGHGYSGMGKQIGMSYAYPYTEQTLLAGNSAKVILEA
319 NPTAAPRESGQVLNKTGSGNGGAYVAFVPAFGIGIVMLANNRNPPEARIKAAHAAILA 1--|
335
379 QLAG 1
-----
1 match found in sequence:
q99tr1 : Hypothetical protein SAV1588.
(from "lactxs_spt.pep")
TOIG of: q99tr1 check: 953 from: 1 to: 733
ID 099TR1 PRELIMINARY; PRT; 733 AA.
AC 099TR1;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical protein SAV1588.

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GN SAV1588 OR SA1416.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952, PubMed=11410146;
RA Kuroda M., Ohca T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003362; BAB57750.1; -
DR EMBL; AP003134; BAB42680.1; -
DR InterPro: IPR001279; Bactamase-like.
DR InterPro: IPR004477; ComEC_N-term.
DR InterPro: IPR004797; ComEC_Rec2.
DR Pfam: PF00753; lactamase_B; 1.
DR TIGRFAMS: TIGR00360; ComEC_N-term; 1.
DR TIGRFAMS: TIGR00361; ComEC_Rec2; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 733 AA; 84997 MW; 783F23BAC38D3A02 CRC64;
...
099TR1 Length: 733 March 17, 2003 12:32 Type: P Check: 953
Found using 'KTXS' (swope073.key)
...
609 KNEYSIITMYQNKVKLLMGDAKNNESLLKKNLPEDILKVGHGKSTSRKEFIE 1--|
659
669 MIKPKISLSSCKNNMYHLPNIEYVKRLQIRSRILYNSQNGQV
-----
1 match found in sequence:
q9aifg7 : Class C beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q9aifg7 check: 9615 from: 1 to: 381
ID 09AEG7 PRELIMINARY; PRT; 381 AA.
AC 09AEG7;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Class C beta-lactamase.
GN AMPC.
OS Citrobacter freundli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC:8454;
RA Barlow M., Hall B.G.;
RT "Origin and Evolution of the ampc b-lactamases of Citrobacter
freundlii."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349570; AAK32688.1; -
DR HSSP; P00811; 1C3B.
DR InterPro: IPR001465; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.

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DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 41948 MW; B5AC0DBB81FD0742 CRC64;

09AGF7 length: 381 March 17, 2003 12:32 Type: P Check: 9615 ..
Found using 'KTXS' (swope073.key)

285 MYGIGLWMLNPLKADSIINGSDSKVALALPAVEVNPAPAVKASVHKTGSGTGFSGS
335

345 YVAFVPEKNLGIWMLANKSYNPAPVPEAAMRILEKIQ

1 match found in sequence:
q9afg8 : Class C beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q9afg8 check: 668 from: 1 to: 381

ID 09AFG8 PRELIMINARY; PRT; 381 AA.
AC 09AFG8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Class C beta-lactamase.
GN AMPC.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC:6879;
RA Barlow M., Hall B.G.;
RT "Origin and Evolution of the ampc b-lactamases of Citrobacter
freundii."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349569; AKK32687.1; -
DR HSSP; P00811; IC3B.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 42057 MW; 626D564722059D18 CRC64;

09AFG8 length: 381 March 17, 2003 12:32 Type: P Check: 668 ..
Found using 'KTXS' (swope073.key)

285 MYGIGLWMLNPLKADSIINGSDSKVALALPAVEVNPAPAVKASVHKTGSGTGFSGS
335

345 YVAFVPEKNLGIWMLANKSYNPAPVPEAAMRILEKIQ

1 match found in sequence:
q9afg9 : Class C beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q9afg9 check: 2465 from: 1 to: 378

ID 09AGT9 PRELIMINARY; PRT; 378 AA.
AC 09AGT9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Class C beta-lactamase.
GN AMPC.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.

OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=520R;
RA Raimondi A., Sisto F., Nikaido H.;
RT "A mutation in Serratia marcescens AmpC beta-lactamase producing high-
level resistance to ceftazidime and cefipime."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327325; AKK15702.1; -
DR HSSP; P05364; 2BLT.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 378 AA; 41244 MW; AB621C271E9C5677 CRC64;

09AGT9 length: 378 March 17, 2003 12:32 Type: P Check: 2465 ..
Found using 'KTXS' (swope073.key)

280 FTQDLMMENYYPVKLSRLIEGNMAGMNGTPATAITPPPELIRAGWYKTKGSGTGFST
330

340 YAVFIPAKNIYVWMLANKWFPNDRVPAHYHVOALEKR

1 match found in sequence:
q9agu0 : Class C beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q9agu0 check: 2784 from: 1 to: 378

ID 09AGU0 PRELIMINARY; PRT; 378 AA.
AC 09AGU0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Class C beta-lactamase.
GN AMPC.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S3;
RA Raimondi A., Sisto F., Nikaido H.;
RT "A mutation in Serratia marcescens AmpC beta-lactamase producing high-
level resistance to ceftazidime and cefipime."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327324; AKK15701.1; -
DR HSSP; P05364; 2BLT.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 378 AA; 41232 MW; 896BEFE72AF483FE CRC64;

09AGU0 length: 378 March 17, 2003 12:32 Type: P Check: 2784 ..
Found using 'KTXS' (swope073.key)

280 FTQDLMMENYYPVKLSRLIEGNMAGMNGTPATAITPPPELIRAGWYKTKGSGTGFST
330

340 YAVFIPAKNIYVWMLANKWFPNDRVPAHYHVOALEKR

1 match found in sequence:
q9afj3 : Telchoic acid phosphorylcholine esterase precursor.

```

(from "lactxs_spt.pep")
TOIG of: q9ajf3 check: 6889 from: 1 to: 627

ID 09AJU3 PRELIMINARY; PRT; 627 AA.
AC 09AJU3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Teichoic acid phosphorylcholine esterase precursor.
GN PCE.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R36A;
RX MEDLINE=21160195; PubMed=11260477;
RA Vollmer W., Tomasz A.;
RT "Identification of the teichoic acid phosphorylcholine esterase in
RT Streptococcus pneumoniae."
RL MOL. Microbiol. 39:1610-1622(2001).
DR EMBL: AJ293572; CAC29434.1;
DR InterPro: IPR001279; Blactamase-like.
DR InterPro: IPR002479; CW_binding.
DR Pfam: PF01473; CW_binding_1; 9.
DR Pfam: PF00753; Lactamase_B; 1.
KW SIGNAL.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 627 TEICHOIC ACID PHOSPHORYLCHOLINE ESTERASE.
SQ SEQUENCE 627 AA; 72118 MW; 6B309D30177369F5 CRC64;

Q9AJU3 Length: 627 March 17, 2003 12:32 Type: P Check: 6889
Found using 'KTxs' (swope073.key)

...

520 AVGIWKDKWYFLKENGQLLVNGKTPPEGYTVDSGAMLVDSIEKSATIKTSHSEIKE |--|
570

560 SKEVYKDKLENKETSQHESVTNFSTSDLTSTSSQSETSVKNK

...

1 match found in sequence:
q9ajw1; Methyl parathion hydrolase.
(from "lactxs_spt.pep")
TOIG of: q9ajw1 check: 1592 from: 1 to: 331

ID 09AJW1 PRELIMINARY; PRT; 331 AA.
AC 09AJW1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Methyl parathion hydrolase.
GN MPD.
OS Plesiomonas sp. M6.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Plesiomonas.
OX NCBI_TaxID=153154;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M6;
RX MEDLINE=21455057; PubMed=11571204;
RA Cul Z., Li S., Fu G.;
RT "Isolation of Methyl Parathion-Degrading Strain M6 and Cloning of the
RT Methyl Parathion Hydrolase Gene."
RL Appl. Environ. Microbiol. 67:4922-4925(2001).
DR EMBL: AF338729; AKK14390.1;
DR InterPro: IPR001969; Aspartate-ase_site.
DR InterPro: IPR001279; Blactamase-like.

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DR Pfam: PF00753; Lactamase_B; 1.
DR PROSITE, PS00141; ASP_PROTEASE; UNKNOWN_1.
DR Hydrolyase.
SQ SEQUENCE 331 AA; 34882 MW; 623A356021162056 CRC64;

Q9AJW1 Length: 331 March 17, 2003 12:32 Type: P Check: 1592
Found using 'KTxs' (swope073.key)

...

29 LVSTAHAAAPQVRTSAPGYRMLIGDEFITALSDGVALPYDKRLNPAPRTOSALAKSF |--|
79 82

89 QKAPLETSVTGYLVNTGSKLVVDTGAAAGLEPTLGRLANLKA

...

1 match found in sequence:
q9amj6; Extended spectrum beta-lactamase VEB-1b.
(from "lactxs_spt.pep")
TOIG of: q9amj6 check: 6157 from: 1 to: 299

ID 09AMJ6 PRELIMINARY; PRT; 299 AA.
AC 09AMJ6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Extended spectrum beta-lactamase VEB-1b.
GN BLA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RA Poliel L., Kotliar V.O., Mokaddas E.M., Karim A., Nordmann P.;
RT "VEB-1 like extended spectrum beta-lactamases in Pseudomonas
RT aeruginosa from Kuwait."
RL Emerging Infect. Dis. 0:0-0(2001).
DR EMBL: AF324834; AAK14294.1;
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase.
DR Pfam: PF00144; Beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
SQ SEQUENCE 299 AA; 33750 MW; 7D4B14FACEFA2D7B CRC64;

Q9AMJ6 Length: 299 March 17, 2003 12:32 Type: P Check: 6157
Found using 'KTxs' (swope073.key)

...

53 KOTLIKINDFHPMQSVKFPFIALAVLSEIDKGNLSFQKIEITPPQDLLPTWSPIRKEEF |--|
103

113 PNGTLLIEIILNTVSESDNIGCDILKLGIGTDSVOKFLNAN

...

1 match found in sequence:
q9amj7; Extended spectrum beta-lactamase VEB-1a.
(from "lactxs_spt.pep")
TOIG of: q9amj7 check: 6480 from: 1 to: 299

ID 09AMJ7 PRELIMINARY; PRT; 299 AA.
AC 09AMJ7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

```

DE Extended spectrum beta-lactamase YEB-1a.
 GN BLA.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Polirel L., Rotimi V.O., Mokaddas E.M., Karim A., Nordmann P.;
 RT "YEB-1 like extended spectrum beta-lactamases in Pseudomonas
 aeruginosa from Kuwait.",
 RL Emerging Infect. Dis. 0:0-0(2001).
 DR EMBL; AF324833; AKI4293.1; -
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PRINTS: PR00118; B_LACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
 SQ SEQUENCE 299 AA; 33721 MW; 799DA995C4898AAB CRC64;

Q9AMJ7 Length: 299 March 17, 2003 12:32 Type: P Check: 6480
 Found using 'KTXS' (swope073.key)

53 KDTLKINDFHFMQSVMKFPIALAVLSEIDKGNLSFEQKIETPTQDLLPKTWSPIKKEEF
 1--1
 103

113 PNGTITITEQIINVTYVESDNIQCILILKLGITDSVQKFLNAN

1 match found in sequence:
 g9c6r4 ; Competence protein ComEC.
 (from "lactxs_spt.pep")
 TOIG of: g9c6r4 check: 1739 from: 1 to: 736

ID Q9C6R4 PRELIMINARY; PRT; 736 AA.
 AC Q9C6R4
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Competence protein ComEC.
 GN COMEC OR LI1772.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403.
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Manger S., Jallion O., Malarne K.,
 Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 lactis ssp. lactis IL1403.",
 RL Genome Res. 11:731-753(2001).
 DR EMBL; AE006407; AAK05870.1; -
 DR InterPro: IPR001279; Blactamase-like.
 DR InterPro: IPR004477; ComEC_N-term.
 DR InterPro: IPR004797; ComEC_N-term.
 DR Pfam: PF00753; lactamase_B; 1.
 DR TIGRPFAMS: TIGR00360; ComEC_N-term; 1.
 DR TIGRPFAMS: TIGR00361; ComEC_N-term; 1.
 KW Complete proteome.
 SQ SEQUENCE 736 AA; 84380 MW; 1AB4D93329AF5D09 CRC64;

Q9C6R4 Length: 736 March 17, 2003 12:32 Type: P Check: 1739
 Found using 'KTXS' (swope073.key)

618 DNNDIYVYGNFYHFKFLFTGDLREGEKELKNPKIKVLYKVGHHGSKTSSNPDFIK
 1--1
 668
 678 EINPKLALISVGEKNRYGHPNQETLETLKKNQIRILFTDQKAL

1 match found in sequence:
 g9c124 ; Hypothetical protein yfci.
 (from "lactxs_spt.pep")
 TOIG of: g9c124 check: 3753 from: 1 to: 210

ID Q9C124 PRELIMINARY; PRT; 210 AA.
 AC Q9C124;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein yfci.
 GN yfci OR LI0542.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Manger S., Jallion O., Malarne K.,
 Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 lactis ssp. lactis IL1403.",
 RL Genome Res. 11:731-753(2001).
 DR EMBL; AE006288; AAK04640.1; -
 DR InterPro: IPR001279; Blactamase-like.
 DR Pfam: PF00753; lactamase_B; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 210 AA; 23732 MW; D2348872511D0EF1 CRC64;

Q9C124 Length: 210 March 17, 2003 12:32 Type: P Check: 3753
 Found using 'KTXS' (swope073.key)

1 MKIKYVKNIAQENTYLLNSSTSHLITDPSGSALLERLKTKDTKSTAILTTHAFDHI
 1--1
 45 48

61 IGLNELRKHFDPVPIYLSAEKEWKNPKLNASPFILG

1 match found in sequence:
 g9eur5 ; Teichoic acid phosphorylcholine esterase precursor.
 (from "lactxs_spt.pep")
 TOIG of: g9eur5 check: 6869 from: 1 to: 627

ID Q9EUR5 PRELIMINARY; PRT; 627 AA.
 AC Q9EUR5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Teichoic acid phosphorylcholine esterase precursor.
 GN LYTD.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R6;
 RA de las Rivas B., Garcia J.L., Lopez R., Garcia P.;

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RT "Isolation, cloning and expression of the lylD gene encoding the
RT pneumococcal teichoic phosphorylcholine esterase."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ272039; CAC20935.1; -.
DR InterPro: IPR001279; Bactamase-like.
DR InterPro: IPR002479; CW_binding.
DR Pfam: PF01473; CW_binding_1; 9.
DR Pfam: PF00753; lactamase_B; 1.
KW Signal.
FT SIGNAL 1 25
FT CHAIN 26 627 TEICHOIC ACID PHOSPHORYLCHOLINE ESTERASE.
SQ SEQUENCE 627 AA; 72104 MW; 3132F0A3FE14CF6 CRC64;
-----
Q9EUR5 Length: 627 March 17, 2003 12:32 Type: P Check: 6869 ..
Found using 'KTXS' (swope073.key)

520 AVGWIKDKWYFLKENGQLVNGKTPGYTVDSGAMLVDSIEKSATIKTSHSEIKE
|---|
570

560 SKEVYKDKLENKETSQHESVTNFSTSDILNISTQSSETSVYKNS
-----
1 match found in sequence:
q9ex97 : AmpC beta-lactamase class C.
(from 'lacktxs_spt.pep')
TOIG of: q9ex97 check: 1681 from: 1 to: 390

ID Q9EX97 PRELIMINARY; PRT; 390 AA.
AC Q9EX97;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE AmpC beta-lactamase class C.
GN AMPC.
OS Ochrobactrum anthropl.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Ochrobactrum.
OX NCBI_TaxID=529;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SLO 74;
RX MEDLINE=21344625; PubMed=11451692;
RA Nadjar D., Labia R., Cerceau C., Bizet C., Philippou A., Arlet G.;
RT "Molecular characterization of chromosomal class C beta-lactamase and
RT its regulatory gene in Ochrobactrum anthropl."
RL Antimicrob. Agents Chemother. 45:2324-2330(2001).
DR EMBL: AJ401618; CAC04522.1; -.
DR HSSP: P05364; 2BLT.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 390 AA; 42275 MW; 452C897D68C91082 CRC64;
-----
Q9EX97 Length: 390 March 17, 2003 12:32 Type: P Check: 1681 ..
Found using 'KTXS' (swope073.key)

351 YAAFIAPAKTGIIVLANRNPIDERYKAAVRIIQLALDNKO
|---|
341

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1 match found in sequence:
q9ex99 : beta-lactamase class C.

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(from 'lacktxs_spt.pep')
TOIG of: q9ex99 check: 2322 from: 1 to: 390

ID Q9EX99 PRELIMINARY; PRT; 390 AA.
AC Q9EX99;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta-lactamase class C.
GN BLA OCH-7.
OS Ochrobactrum anthropl.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Ochrobactrum.
OX NCBI_TaxID=529;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-103952;
RA Nadjar D., Labia R., Cerceau C., Bizet C., Philippou A., Arlet G.;
RT "Molecular characterization of the chromosomal class C ss-lactamase
RT and its regulatory gene in Ochrobactrum anthropl."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ295345; CAC17627.1; -.
DR HSSP: P05364; 2BLT.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 390 AA; 42290 MW; 44814E1108AFCD27 CRC64;
-----
Q9EX99 Length: 390 March 17, 2003 12:32 Type: P Check: 2322 ..
Found using 'KTXS' (swope073.key)

291 NNOGLGMEFYNYPTALKTLLAGNSSDMALKSHKIKKFTPPROPASDVNLNKGSTNGFGA
|---|
341

351 YAAFIAPAKTGIIVLANRNPIDERYKAAVRIIQLALDNKO
|---|
341

-----
1 match found in sequence:
q9exa0 : Beta-lactamase class C.
(from 'lacktxs_spt.pep')
TOIG of: q9exa0 check: 1800 from: 1 to: 390

ID Q9EXA0 PRELIMINARY; PRT; 390 AA.
AC Q9EXA0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta-lactamase class C.
GN BLA OCH-6.
OS Ochrobactrum anthropl.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Ochrobactrum.
OX NCBI_TaxID=529;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-103949;
RA Nadjar D., Labia R., Cerceau C., Bizet C., Philippou A., Arlet G.;
RT "Molecular characterization of the chromosomal class C ss-lactamase
RT and its regulatory gene in Ochrobactrum anthropl."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ295344; CAC17626.1; -.
DR HSSP: P00811; 1C3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 390 AA; 42347 MW; A3B96462610ADF05 CRC64;
-----
Q9EXA0 Length: 390 March 17, 2003 12:32 Type: P Check: 1800 ..

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Found using 'KTXS' (swope073.key)

291 NNOGLGWEFYNYPTALKTLLAGNSSDMAKSHKIEKEDTPROPSADVWLKNTGSGTNGFGA
341

351 YAAFIPAKKIGIVLLANRNPIDERVKAAYRILOALDNKQ

1 match found in sequence:

q9exa1 ; Beta-lactamase class C.

(from "lactxs_spt.pep")

TOIG of: q9exa1 check: 1544 from: 1 to: 390

ID Q9EXA1 PRELIMINARY; PRT; 390 AA.

AC Q9EXA1; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

GN BLA OCH-5.

OS Ochrobactrum anthropi.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Brucellaceae; Ochrobactrum.

OX NCBI_TaxID=529;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=102332;

RA Nadjar D., Labia R., Cerceau C., Bizet C., Philippin A., Arlet G.;

RT "Molecular Characterization of the Chromosomal Class C ss-lactamase

and its regulatory gene in Ochrobactrum anthropi.";

RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ295343; CACI7625.1; -

DR HSSP: P05364; 2BLT.

DR InterPro: IPR001466; Beta_lactamase.

DR InterPro: IPR001586; Beta_lactamase.C.

DR Pfam: PF00144; beta-lactamase; 1.

DR PROSITE: PS00336; BETA_LACTAMASE.C; 1.

SQ SEQUENCE 390 AA; 42326 MW; 6716D86B08F50311 CRC64;

Q9EXA1 Length: 390 March 17, 2003 12:32 Type: P Check: 1544

Found using 'KTXS' (swope073.key)

291 NNOGLGWEFYNYPTALKTLLAGNSSDMAKSHKIEKEDTPROPSADVWLKNTGSGTNGFGA
341

351 YAAFIPAKKIGIVLLANRNPIDERVKAAYRILOALDNKQ

1 match found in sequence:

q9exa2 ; Beta-lactamase class C.

(from "lactxs_spt.pep")

TOIG of: q9exa2 check: 1159 from: 1 to: 390

ID Q9EXA2 PRELIMINARY; PRT; 390 AA.

AC Q9EXA2; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

GN BLA OCH-4.

OS Ochrobactrum anthropi.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Brucellaceae; Ochrobactrum.

OX NCBI_TaxID=529;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=82116;

RA Nadjar D., Labia R., Cerceau C., Bizet C., Philippin A., Arlet G.;

RT "Molecular Characterization of the Chromosomal Class C ss-lactamase

and its regulatory gene in Ochrobactrum anthropi.";

RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ295342; CACI7624.1; -

DR HSSP: P05364; 2BLT.

DR InterPro: IPR001466; Beta_lactamase.

DR InterPro: IPR001586; Beta_lactamase.C.

DR Pfam: PF00144; beta-lactamase; 1.

DR PROSITE: PS00336; BETA_LACTAMASE.C; 1.

SQ SEQUENCE 390 AA; 42258 MW; 9154D0D1EB71A40A CRC64;

Q9EXA2 Length: 390 March 17, 2003 12:32 Type: P Check: 1159

Found using 'KTXS' (swope073.key)

291 NNOGLGWEFYNYPTALKTLLAGNSSDMAKSHKIEKEDTPROPSADVWLKNTGSGTNGFGA
341

351 YAAFIPAKKIGIVLLANRNPIDERVKAAYRILOALDNKQ

1 match found in sequence:

q9exa3 ; Beta-lactamase class C.

(from "lactxs_spt.pep")

TOIG of: q9exa3 check: 1631 from: 1 to: 390

ID Q9EXA3 PRELIMINARY; PRT; 390 AA.

AC Q9EXA3; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

GN BLA OCH-3.

OS Ochrobactrum anthropi.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Brucellaceae; Ochrobactrum.

OX NCBI_TaxID=529;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=82115 T;

RA Nadjar D., Labia R., Cerceau C., Bizet C., Philippin A., Arlet G.;

RT "Molecular Characterization of the Chromosomal Class C ss-lactamase

and its regulatory gene in Ochrobactrum anthropi.";

RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ295341; CACI7623.1; -

DR HSSP: P00811; 1C3B.

DR InterPro: IPR001466; Beta_lactamase.

DR InterPro: IPR001586; Beta_lactamase.C.

DR Pfam: PF00144; beta-lactamase; 1.

DR PROSITE: PS00336; BETA_LACTAMASE.C; 1.

SQ SEQUENCE 390 AA; 42440 MW; E273CF3E0DC21B14 CRC64;

Q9EXA3 Length: 390 March 17, 2003 12:32 Type: P Check: 1631

Found using 'KTXS' (swope073.key)

291 NNOGLGWEFYNYPTALKTLLAGNSSDMAKSHKIEKEDTPROPSADVWLKNTGSGTNGFGA
341

351 YAAFIPAKKIGIVLLANRNPIDERVKAAYRILOALDNKQ

1 match found in sequence:

q9exa4 ; Beta-lactamase class C.

(from "lactxs_spt.pep")

TOIG of: q9exa4 check: 2072 from: 1 to: 390

ID Q9EXA4 PRELIMINARY; PRT; 390 AA.

AC Q9EXA4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta-lactamase class C.
 GN BLA OCH-2.
 OS Ochrobactrum anthropi.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Ochrobactrum.
 OC NCBI_TaxID=529;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-82113;
 RA Nadar D., Labia R., Cerceau C., Bizet C., Philippou A., Arlet G.;
 RT "Molecular Characterization of the Chromosomal Class C ss-lactamase
 RT and its regulatory gene in Ochrobactrum anthropi.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ295340; CAC17622.1; -.
 DR HSSP; P05364; 2BLT.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR001586; Beta_lactamase_C.
 DR Pfam; PF00144; beta-lactamase; 1.
 DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 390 AA; 42307 MW; 253ECE4P9594FCD CRC64;

Q9EXA4 Length: 390 March 17, 2003 12:32 Type: P Check: 2072 ..
 Found using 'KTXS' (swope073.key)

291 NNOGLGWEFYNYPTALKTLLAGNSDMALKSHKIEKEDTTPROPSADYWLNTGSGTNGFGA 1--1
 341

351 YAAFIPAKKTGIVLIANNRYPIDERIKARVITLQALDNKQ

1 match found in sequence:
 q9exv5; Beta-lactamase UOE-1 (cefotaxime-hydrolyzing beta-lactamase,
 (from "lactxs_spt.pep")
 ToIG of: q9exv5 check: 348 from: 1 to: 291

ID Q9EXV5 PRELIMINARY; PRT; 291 AA.
 AC Q9EXV5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta-lactamase UOE-1 (cefotaxime-hydrolyzing beta-lactamase,
 DE CTX-M-11).
 GN BLA UOE-1 OR BLA CTX-M-15 OR BLA.
 OS Escherichia coli.
 OC Plasmid pMTE001, and plasmid pBLACTX-M-11.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-SEC124; PLASMID=pMTE001;
 RA Muratani T., Takahashi K., Matsumoto T.;
 RT "Isolation of beta-lactam high-resistant Escherichia coli strains
 RT carrying a new ESBL UOE-1 (CTX-M-3 like beta-lactamase).";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21363408; PubMed=11470367;
 RA Karim A., Polirel L., Nagarajan S., Nordmann P.;
 RT "Plasmid-mediated extended-spectrum beta-lactamase (CTX-M-3 like) from
 RT India and gene association with insertion sequence ISEcp1.";
 RL FEMS Microbiol. Lett. 201:237-241(2001).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN-CLIS 3551/98; PLASMID=BLACTX-M-11;
 RA Gutadkowski M.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN-CLIS 3551/98; PLASMID=BLACTX-M-11;
 RA Baraniak A.;
 RL Thesis (2001), Department of Molecular Microbiology,
 RL Sera & Vaccines Central Research Laboratory, Warsaw, Poland.
 DR EMBL; AY013478; AAG48377.1; -.
 DR EMBL; AY044436; AAL02127.1; -.
 DR EMBL; AJ310929; CAC84572.1; -.
 DR HSSP; Q47066; 1BZA.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; beta-lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Plasmid.
 SQ SEQUENCE 291 AA; 31143 MW; 49C531A7D5607BA4 CRC64;

Q9EXV5 Length: 291 March 17, 2003 12:32 Type: P Check: 348 ..
 Found using 'KTXS' (swope073.key)

187 RANAQTLRLTLGKALGDSORADLYTMKGNTTGAASIGLPAWVYGDKTSGGYGT 1--1
 237
 247 NDIAVTPKDRAPLILVTFYTPQPKAESRDOVLASAAKIYVDG

1 match found in sequence:
 q9ezq7; Class A beta-lactamase AST-1.
 (from "lactxs_spt.pep")
 ToIG of: q9ezq7 check: 9722 from: 1 to: 310

ID Q9EZQ7 PRELIMINARY; PRT; 310 AA.
 AC Q9EZQ7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Class A beta-lactamase AST-1.
 GN BLA.
 OS Nocardia asteroides.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Nocardia.
 OC NCBI_TaxID=1824;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21091887; PubMed=11181374;
 RA Polirel L., Laurent F., Neas T., Labia R., Bolron P., Nordmann P.;
 RT "Molecular and Biochemical Analysis of AST-1, a Class A beta-Lactamase
 RT from Nocardia asteroides Sensu Stricto.";
 RL Antimicrob. Agents Chemother. 45:878-882(2001).
 DR EMBL; AF279904; AAG44836.1; -.
 DR HSSP; P14559; 1BSG.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; beta-lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 SQ SEQUENCE 310 AA; 32475 MW; 53668F7DBFF1A6B3 CRC64;

Q9EZQ7 Length: 310 March 17, 2003 12:32 Type: P Check: 9722 ..
 Found using 'KTXS' (swope073.key)

205 AALADYBALVGDVLCAPERDQLKAMLVANTGTATIRAGLPADWTVDKTSPPAYGSA 1--1
 255


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265      LDVAVMPGRAPYIAVLSTKSEDAEPDALLAEATRVVDA
...
-----
1 match found in sequence:
  q9f0v2 ; Beta-lactamase OXA-26.
  (from "lactxs_spt.pep")
  TOIG of: q9f0v2 check: 1911 from: 1 to: 275

ID      Q9F0V2      PRELIMINARY;      PRT;      275 AA.
AC      Q9F0V2;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      Beta-lactamase OXA-26.
GN      BLA-OXA26.
OS      Acinetobacter baumannii.
OC      Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC      Acinetobacter.
OX      NCBI_TaxID=470;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=04737;
RA      MEDLINE=21091835; PubMed=11158758;
RT      "Afzal-Shah M., Woodford N., Livermore D.M.;
RT      "Characterization of OXA-25, OXA-26 and OXA-27, molecular class D
RT      beta-lactamases associated with carbapenem resistance in clinical
RT      isolates of Acinetobacter baumannii."
RL      Antimicrob. Agents Chemother. 45:583-588(2001).
DR      EMBL; AF201827; AAC35608.1; -.
DR      HSSP; P14489; 1E3U
SQ      SEQUENCE 275 AA; 30953 MW; 5FAE22A6F1ABC62B CRC64;

Q9F0V2 Length: 275 March 17, 2003 12:32 Type: P Check: 1911 ..
Found using 'KTXS' (swope073.key)

1      MKKFLIPFISILVLSACSSIKTKSEDPNHNHSSQHEKAIKSYFDEAQTGVIITKEG
      24 27

61      KNLSTYGNALRANKY
...
-----
1 match found in sequence:
  q9f0v3 ; Beta-lactamase OXA-25.
  (from "lactxs_spt.pep")
  TOIG of: q9f0v3 check: 1416 from: 1 to: 275

ID      Q9F0V3      PRELIMINARY;      PRT;      275 AA.
AC      Q9F0V3;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      Beta-lactamase OXA-25.
GN      BLA-OXA25.
OS      Acinetobacter baumannii.
OC      Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC      Acinetobacter.
OX      NCBI_TaxID=470;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=327009;
RA      MEDLINE=21091835; PubMed=11158758;
RT      "Afzal-Shah M., Woodford N., Livermore D.M.;
RT      "Characterization of OXA-25, OXA-26 and OXA-27, molecular class D
RT      beta-lactamases associated with carbapenem resistance in clinical
RT      isolates of Acinetobacter baumannii."
RL      Antimicrob. Agents Chemother. 45:583-588(2001).
DR      EMBL; AF201826; AAC35607.1; -.

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DR      HSSP; P14489; 1E3U.
SQ      SEQUENCE 275 AA; 30966 MW; 9CA39C10AC107039 CRC64;

Q9F0V3 Length: 275 March 17, 2003 12:32 Type: P Check: 1416 ..
Found using 'KTXS' (swope073.key)

1      MKKFLIPFISILVLSACSSIKTKSEDPNHNHSSQHEKAIKSYFDEAQTGVIITKEG
      24 27

61      KNLSTYGNALRANKY
...
-----
1 match found in sequence:
  q9f279 ; L2 beta-lactamase.
  (from "lactxs_spt.pep")
  TOIG of: q9f279 check: 2870 from: 1 to: 303

ID      Q9F279      PRELIMINARY;      PRT;      303 AA.
AC      Q9F279;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      L2 beta-lactamase.
GN      BLA/L2.
OS      Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
OC      maltophilia).
OC      Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC      Stenotrophomonas.
OX      NCBI_TaxID=40324;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=UDA-511;
RA      MEDLINE=20106971; PubMed=10639352;
RT      Zhang L., Li X.Z., Poole K.;
RT      "Multiple antibiotic resistance in Stenotrophomonas maltophilia:
RT      involvement of a multidrug efflux system."
RL      Antimicrob. Agents Chemother. 44:287-293(2000).
DR      EMBL; AF299368; AGL3585.1; -.
DR      HSSP; Q47066; 1BZA.
DR      InterPro; IPR001466; Beta_lactamase.
DR      InterPro; IPR000871; Beta_lactamase_A.
DR      Pfam; PF00144; beta_lactamase; 1.
DR      PRINTS; PR00118; BLACTAMASEA.
DR      PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
SQ      SEQUENCE 303 AA; 32012 MW; AFB82036AA042251 CRC64;

Q9F279 Length: 303 March 17, 2003 12:32 Type: P Check: 2870 ..
Found using 'KTXS' (swope073.key)

...
197      AAMATLQRYVLGEVLPASRQQLADWLIDNENGDACLRAGLGKRRVGDGKSNEDAR
      247

257      NDIATVLPVAGAPWVLTAYLQAGAISYBQASVLAQVGRIDR
...
-----
1 match found in sequence:
  q9f2k7 ; Putative beta-lactamase related protein.
  (from "lactxs_spt.pep")
  TOIG of: q9f2k7 check: 4588 from: 1 to: 292

ID      Q9F2K7      PRELIMINARY;      PRT;      292 AA.
AC      Q9F2K7;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)

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DE Putative beta-lactamase related protein.
GN SC03774 OR SCH63.21.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Crozin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke I., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitz E., Rajadream M.A., Rutherford K., Rutter S., Taylor K.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL442629; CACI0312.1;
SQ SEQUENCE 292 AA; 30731 MW; 1110379C0157447A CRC64;

09F2K7 Length: 292 March 17, 2003 12:32 Type: P Check: 4588 ..
Found using 'KTXS' (swope073.key)

...

184 RDMTRLGAVWRDEACPEYGAAMRRIMGLWPHRLASGFPDDVHAKGTSPLTRN
234
244 EVGVVEYPDGGRVAVFTRTAHTAATVPAADAVTGAARIADV

-----
1 match found in sequence:
q9f3z2 : Cephalosporinase.
(from "lacks_spt.pep")
TOIG of: q9f3z2 check: 1955 from: 1 to: 390

ID Q9F3Z2 PRELIMINARY; PRT; 390 AA.
AC Q9F3Z2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cephalosporinase.
GN AMPC.
OS Ochrobactrum anthropi.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Ochrobactrum.
OX NCBI_TaxID=529;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2171;
RX MEDLINE=21282824; PubMed=11389106;
RA Higgins C.S., Avison M.B., Jamieson L., Simm A.M., Bennett P.M.,
RA Walsh T.R.;
RT "Characterization, cloning and sequence analysis of the inducible
RT Ochrobactrum AmpC beta-lactamase.";
RL J. Antimicrob. Chemother. 47:745-754(2001).
DR EMBL; AJ299421; CACI17149.1;
DR HSSP; P05364; 2BLT.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase.C.
DR Pfam; PF00144; beta_lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Porin.
SQ SEQUENCE 390 AA; 42298 MW; 7CD2D963B39024A9 CRC64;

09F3Z2 Length: 390 March 17, 2003 12:32 Type: P Check: 1955 ..

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Found using 'KTXS' (swope073.key)

...

291 NNOGLGWEFYNYPTALKTLIAGNSDMLKSHKIEKFTPTPROPSADVWMLNTGSGNGGA
341
351 YAAFIPAKTKGIVLANRNYPIDERVKAAYRIQLADMKQ

-----
1 match found in sequence:
q9f491 : Class C beta-lactamase.
(from "lacks_spt.pep")
TOIG of: q9f491 check: 134 from: 1 to: 381

ID Q9F491 PRELIMINARY; PRT; 381 AA.
AC Q9F491;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Class C beta-lactamase.
GN AMPC.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ODHYP;
RX MEDLINE=21100285; PubMed=11179650;
RA Barnaud G., Labie R., Raskine L., Sanson-Le Pors M., Philippou A.,
RA Arlet G.;
RT "Extension of resistance to cefepime and ceftipime associated to a six
RT amino acid deletion in the H-10 helix of the cephalosporinase of an
RT Enterobacter cloacae clinical isolate.";
RL FEMS Microbiol. Lett. 195:185-190(2001).
DR EMBL; AJ278995; CAC08446.1;
DR HSSP; P05364; 2BLT.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase.C.
DR Pfam; PF00144; beta_lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 381 AA; 41271 MW; CA9AF09300CDEA9C CRC64;

09F491 Length: 381 March 17, 2003 12:32 Type: P Check: 134 ..
Found using 'KTXS' (swope073.key)

...

285 MYGGLGWEMLNMPVEANTVIEGSDSKVALAPLVAEVPAPPAVEASVWHTGSGSGFS
335
345 YVAFIPEKQIGIVMLANKSYNPAPPAVEAHTLDALQ

-----
1 match found in sequence:
q9f493 : Class C beta-lactamase.
(from "lacks_spt.pep")
TOIG of: q9f493 check: 6296 from: 1 to: 375

ID Q9F493 PRELIMINARY; PRT; 375 AA.
AC Q9F493;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Class C beta-lactamase.
GN AMPC.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=550;

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RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CHE:
 RA MEDLINE-21100285; PubMed=11179650;
 RX Barnaud G., Labia R., Raskine L., Sanson-Le Pors M., Philippou A.,
 RA Arlet G.;
 RT "Extension of resistance to cefepime and ceftipime associated to a six
 amino acid deletion in the H-10 helix of the cephalosporinase of an
 RT Enterobacter cloacae clinical isolate.";
 RL FEMS Microbiol. Lett. 195;185-190(2001).
 DR EMBL: AJ278994; CAC08444.1; -
 DR HSSP: P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 375 AA; 40744 MW; B62038B64A128B76 CRC64;
 Q9F493 Length: 375 March 17, 2003 12:32 Type: P Check: 6296 ..
 Found using 'KTXS' (swope073.key)

279 YWRIGMYOGLGEMLMPEVANTVVEGSDPLVVEVNPBPVAVSWYKSTGSGFGS
 329

339 YVAFIEKQIGIVMLANTSYNPARYEAYVHLEALQ

2 matches found in sequence:
 q9f4k3 ; Beta-lactamase FOX-5.
 (from "lacks_spt.pep")
 TOIG of: q9f4k3 check: 8468 from: 1 to: 382

ID Q9F4K3 PRELIMINARY; PRT; 382 AA.
 AC Q9F4K3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-lactamase FOX-5.
 GN FOX-6.
 OS Klebsiella pneumoniae.
 OG plasmid p5064.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID-P5064;
 RA Queenan A.-M., Bush K., Jenkins S.G.;
 RT "A clavulanate-resistant K. pneumoniae clinical isolate encoding
 RT plasmid-mediated TEM-2 like and FOX-5 beta-lactamases.";
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Herrera V.L., Hanson N.D.;
 RT "Fox6, A Novel Plasmid-mediated Ampc Beta-lactamase.";
 RT Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY007369; AAG12974.1; -
 DR EMBL: AY034848; AAK70221.1; -
 DR HSSP: P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW PLASMID.
 SQ SEQUENCE 382 AA; 40882 MW; BBP905F30DEF2B8C CRC64;

Q9F4K3 Length: 382 March 17, 2003 12:32 Type: P Check: 8468 ..
 Found using 'KTXS' (swope073.key)

196 SOTLLPKLHHTTYIQVPESAMVNYAGYSKEDKRVRTPGVLAAMAYGRTGSADLLKF
 246
 256 AEANNGYGDAAVKSALITHTGFSVGMTQGLGWSYAVPYEQTLLAGNAPVAFQ
 316 NPVTRFAVPRKAMGEORLNKTKSGTSGFGAYVAFYPARGIATVMLANRYPLEARVKAHA
 335
 376 ILSQLAE

1 match found in sequence:
 q9f5u0 ; Cefotaxime-hydrolyzing beta-lactamase.
 (from "lacks_spt.pep")
 TOIG of: q9f5u0 check: 9514 from: 1 to: 291

ID Q9F5U0 PRELIMINARY; PRT; 291 AA.
 AC Q9F5U0.
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Cefotaxime-hydrolyzing beta-lactamase.
 OS Klebsiella pneumoniae;
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KPEN216;
 RX MEDLINE=21301175; PubMed=11408239;
 RA Kariuki S., Corhill J.E., Revathi G., Musoke R., Hart C.A.;
 RT "Molecular Characterization of a Novel Plasmid-Encoded Cefotaximase
 RT (CTX-M-12) Found in Clinical Klebsiella pneumoniae Isolates from
 RT Kenya.";
 RL Antimicrob. Agents Chemother. 45:2141-2143(2001).
 DR EMBL: AF305837; AAG34108.1; -
 DR HSSP: Q47066; 1B2A.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 SQ SEQUENCE 291 AA; 31158 MW; 874FEC2917211189 CRC64;

Q9F5U0 Length: 291 March 17, 2003 12:32 Type: P Check: 9514 ..
 Found using 'KTXS' (swope073.key)

187 RAMAQLRLNLTLGKALGDSQRALVYTWKGNLTGASIQAGLPASVWVGKTSQGDVGT
 237

247 NDIAVIMPKRADPILIVYFTQPOPKAESRRDILASAKIVTDS

2 matches found in sequence:
 q9f7u6 ; Carbapenem-hydrolyzing class A beta-lactamase Sme-2.
 (from "lacks_spt.pep")
 TOIG of: q9f7u6 check: 7057 from: 1 to: 294

ID Q9F7U6 PRELIMINARY; PRT; 294 AA.
 AC Q9F7U6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Carbapenem-hydrolyzing class A beta-lactamase Sme-2.
 OS Serratia marcescens.

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OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4126;
RX MEDLINE=20493108; PubMed=11036019;
RA Queenan A.M., Torres-Viera C., Gold H.S., Carmeli Y., Eliopoulos G.M.,
  Moellerling R.C. Jr., Quinn J.P., Hindler J., Medeiros A.A., Bush K.;
  "SME-Type carbapenem-hydrolyzing class A beta-lactamases from
  geographically diverse Serratia marcescens strains.";
  RL Antimicrob. Agents Chemother. 44:3035-3039(2000).
DR EMBL: AF275256; AAG29813.1; -.
DR HSSP: P52663; 1BUU.
DR InterPro: IPR001466; Beta_Lactamase.
DR InterPro: IPR000871; Beta_Lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
SQ SEQUENCE 294 AA; 32276 MW; 7034F1FF770A308B CRC64;

Q9F7U6 Length: 294 March 17, 2003 12:32 Type: P Check: 7057
Found using 'KTXS' (swope073.key)

1 MSNKNVFTASFSVCLATSAFNAHANKSDAAKQIKLEDPDGRIGVFAIDTSGNT
  8 11
61 F
...
188 KAVANSLNKLALGNVLNKKKAIYONMLKNTGDARIRASVPADWVWGKSGCAYGT
  238
248 ANDYAVIWPKNRAPLIVSIYTRKSKODKSHDKTIAEASRLAQ
...
-----
2 matches found in sequence:
q9faa1 : Class C beta-lactamase.
      (from "lactxs_spt.pep")
TOIG of: q9faa1 check: 16 from: 1 to: 382

ID Q9FAA1 PRELIMINARY; PRT; 382 AA.
AC Q9FAA1;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Class C beta-lactamase.
GN BLACMY-9.
OS Escherichia coli.
OC Plasmid pCMXRL.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HKTW68;
RA Doi Y., Shibata N., Arakawa Y.;
  "Escherichia coli plasmid pCMXRL integron, ampc gene (beta-lactamase
  CMY-9), aacai gene, strain HKTW68.";
  RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DE EMBL: AB061794; BAB72158.1; -.
DR HSSP: P05364; 2BLT.
DR InterPro: IPR001466; Beta_Lactamase.
DR Pfam: PF00144; beta-lactamase; 1.
KW Plasmid.
SQ SEQUENCE 382 AA; 40768 MW; F13315D560CD81C CRC64;

Q9FAA1 Length: 382 March 17, 2003 12:32 Type: P Check: 16
Found using 'KTXS' (swope073.key)

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...
199 EOTLLPGLGMHTTYVNPQAMASYAGYSKEDKPIRVNPGMLADEAVGIRTSADLLAF
  249
259 VKANIGGVDDKALQQAISLTHKGHVSVMGGLGMEYAYPVTEOTLLAGSAKAVILEA
  319
  NPTAPRESGSOVLKNTGSTNGFGAYAFVDPARGIGIVMLANRYPPIPARYKAHAAILA
  335
379 QLAG
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1 match found in sequence:
q9fcw0 : Hypothetical 68.5 kda protein.
      (from "lactxs_spt.pep")
TOIG of: q9fcw0 check: 9177 from: 1 to: 652

ID Q9FCW0 PRELIMINARY; PRT; 652 AA.
AC Q9FCW0;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE Hypothetical 68.5 kda protein.
OS Kluyvera ascorbata.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Kluyvera.
OX NCBI_TaxID=51288;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cip82.95T;
RA Humentik C., Arlet G., Labla R., Philippson A.;
  "Beta-lactamase of Kluyvera ascorbata: progenitor of some plasmid-
  encoded CTX-M types.";
  RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ272538; CAC03614.1; -.
KW Hypothetical protein.
SQ SEQUENCE 652 AA; 68488 MW; 0D378F49E28DC6A3 CRC64;

Q9FCW0 Length: 652 March 17, 2003 12:32 Type: P Check: 9177
Found using 'KTXS' (swope073.key)

592 GLDRMHLGIMAGIGNSQNTKSDVSRHYHSGOYTGISAGITGTWYANPADKTSYLDSWI
  642
652 H
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1 match found in sequence:
q9fmw0 : Genomic DNA, chromosome 5, P1 clone:MLE2.
      (from "lactxs_spt.pep")
TOIG of: q9fmw0 check: 439 from: 1 to: 528

ID Q9FMW0 PRELIMINARY; PRT; 528 AA.
AC Q9FMW0;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Genomic DNA, chromosome 5, P1 clone:MLE2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLDBIA;

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RX MEDLINE=98162728; PubMed=9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned p1 clones."
RL DNA Res. 4:401-414(1997).
DR EMBL: AB007649; BAB08807.1;
DR InterPro: IPR001279; Bactamase-like.
DR Pfam: PF00753; Lactamase_B.1.
DR Pfam: PF02147; UPF0036; 1.
SQ SEQUENCE 528 AA; 58180 MW; D67F7A1613DDA8F CRC64;

Q9FWM0 Length: 528 March 17, 2003 12:32 Type: P Check: 439
Found using 'KTXS' (swope073.key)

173 ITHGHEDHIGALPWIVIPALDPNTPIFASSTFMELIKRLKEHGIFVQSRKTFSTRRRM
|---|
223

233 AGFEIEPTVTHSIPDCSGLPLRCADGNILITGMKIDEAPLD

...
1 match found in sequence:
991775 : Hypothetical protein PA0057.
(from "lactxs_spt.pep")
TOIG of: 991775 check: 8381 from: 1 to: 295

ID 091775 PRELIMINARY; PRT; 295 AA.
AC 091775;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein PA0057.
GN PA0057.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Hickey M.J., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Gainer R.L., Brinkman F.S.L., Huhmagle W.O., Kowalik D.J., Lagrou M.,
RA Brody L.L., Goltzy L., Tolentino E., Westbrock-Wedman S., Yuan Y.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saiter M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:955-964(2000).
EMBL: AE004445; AAC03447.1;
DR InterPro: IPR001279; Bactamase-like.
DR Pfam: PF00753; Lactamase_B.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 295 AA; 32023 MW; 917E56A115D70A54 CRC64;

Q91775 Length: 295 March 17, 2003 12:32 Type: P Check: 8381
Found using 'KTXS' (swope073.key)

30 LRLVYNGEKAIRAVSSELLVIGREAMLIDAFSRADAEQIVKRIQASGCTLSITIVSH
|---|
80 83

90 GDPDFYFGLDVIKAAFPFAKILATAGTVAHQVATKDKAKLAWGCP

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...
1 match found in sequence:
991KB7 : G1/G2 glycoprotein.
(from "lactxs_spt.pep")
TOIG of: 991KB7 check: 8837 from: 1 to: 1135

ID 091KB7 PRELIMINARY; PRT; 1135 AA.
AC 091KB7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE G1/G2 glycoprotein.
OS tomato spotted wilt virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tospovirus.
OX NCBI_Taxid=11613;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D.
RX MEDLINE=21071242; PubMed=11204788;
RA Hofmann K., Qiu W.P., Moyer J.W.;
RT "Overcoming host- and pathogen-mediated resistance in tomato and
RT tobacco maps to the M RNA of Tomato spotted wilt virus."
RL Mol. Plant Microbe Interact. 14:242-249(2001).
DR EMBL: AF208497; AAF80979.1;
DR InterPro: IPR000871; Beta_Lactamase_A.
DR InterPro: IPR005167; Bunya_G1.
DR Pfam: PF03557; Bunya_G1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
SQ SEQUENCE 1135 AA; 127552 MW; 53F271999CABEC33 CRC64;

Q91KB7 Length: 1135 March 17, 2003 12:32 Type: P Check: 8837
Found using 'KTXS' (swope073.key)

53 ENEVPTAASIOREAIETLNVLIESRTPGTRQIREKLTIPISTEPARTKTTISVDLPN
|---|
103

113 NCLNASSLKCEIKIGISTYVNYGVENNGVIYSSVDSAEGLERC

...
1 match found in sequence:
991P6 : L2 b-lactamase.
(from "lactxs_spt.pep")
TOIG of: 991P6 check: 4635 from: 1 to: 303

ID 091P6 PRELIMINARY; PRT; 303 AA.
AC 091P6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE L2 b-lactamase.
GN BIAL2.
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
OS maltophilia).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Stenotrophomonas.
OX NCBI_Taxid=40324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS31;
RX MEDLINE=21091811; PubMed=1158734;
RA Avison M.B., Higgins C.S., von Heldreich C.J., Bennett P.M.,
RA Walsh T.R.;
RT "Plasmid location and molecular heterogeneity of the L1 and L2 beta-
RT lactamase genes from Stenotrophomonas maltophilia."
RL Antimicrob. Agents Chemother. 45:413-419(2001).

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DR EMBL: AJ272110: CAB75347.1; -.
DR HSSP; P00810; ITEM.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN.1.
SQ SEQUENCE 303 AA; 31820 MW; 93BA5698D978406A CRC64;

G9JRP6 Length: 303 March 17, 2003 12:32 Type: P Check: 4635
Found using 'KTXS' (swope073.key)

198 AAMATSLARRAVNGLOPASRROPADWLINDOTGDACLRAGLGRKRRVKGKTSNGDDIR
248
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258 NDIAVLPHAGTAWVTAYVLOGASVDDDORAAVLQVGRYADRM
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RL Antimicrob. Agents Chemother. 44:1470-1478(2000).
DR EMBL; AF180958; AAF86697.1; -.
DR EMBL; AF180957; AAF86696.1; -.
DR HSSP; P00811; 2BLS.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW PorIn.
FT NON_TER 377
SQ SEQUENCE 377 AA; 41269 MW; 336A330610A839E4 CRC64;

O9K373 Length: 377 March 17, 2003 12:32 Type: P Check: 8031
Found using 'KTXS' (swope073.key)

...

291 GKTDLMWEQLPYVSLPDLLTGNDMAMTKSVATPIVPPLPQENVMWINKTSGNGFGA
158
341
351 YIAFVPAKMGIVMLANKNYSIDQRYT

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1 match found in sequence:
g9k4m7; Replication protein.
(from "lactxs_spt.pep")
TOIG of: g9k4m7 check: 5051 from: 1 to: 303

ID O9K4M7 PRELIMINARY; PRT; 303 AA.
AC O9K4M7
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Replication protein.
GN REPX.
OS Staphylococcus haemolyticus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=1283;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NH97A;
RA Antonisen I., Steinum T.M., Sidhu M.S., Sorum H., Sunde M.;
"Organization of the beta-lactamase transposon Tn552, the antiseptic
RT resistant gene qacA and a Staphylococcal insertion Sequence IS257 on
RT large plasmids in multiresistant Staphylococcus haemolyticus.";
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ400722; CAB94811.1; -.
KW Plasmid.
SQ SEQUENCE 303 AA; 35159 MW; 9A936B1AFD0578A9 CRC64;

O9K4M7 Length: 303 March 17, 2003 12:32 Type: P Check: 5051
Found using 'KTXS' (swope073.key)

...

108 SSSIYNDKESQNLGLQNPETIMDSNRSKFGPPEQIILDPNDTJDNDYIKTESNDIDDL
158
168 NDKILTFNNHTNHSNHDNSNFNEALKFOLEELPOSITIONYLS

-----
1 match found in sequence:
g9k593; AmpC beta-lactamase (Fragment).
(from "lactxs_spt.pep")
TOIG of: g9k593 check: 3282 from: 1 to: 238

ID O9K593 PRELIMINARY; PRT; 238 AA.

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AC O9K593;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE AmpC beta-lactamase (Fragment).
GN AMPC.
OS Hafnia alvei.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Hafnia.
OX NCBI_TaxID=569;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HAF Tn1.
RX MEDLINE=20291116; PubMed=10828397;
RA Nadjar D., Rouveau M., Verdet C., Donnay J.L., Herrmann J.L.,
Lagrange P.H., Philippou A., Arlet G.;
"Outbreak of Klebsiella pneumoniae producing transferable AmpC-type
RT beta-lactamase (ACC-1) originating from Hafnia alvei.";
RL FEMS Microbiol. Lett. 187:35-40(2000).
DR EMBL; AJ270941; CAB66897.1; -.
DR HSSP; P00811; 2BLS.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; beta-lactamase; 1.
FT NON_TER 238
SQ SEQUENCE 238 AA; 26097 MW; 8B7C2D0336514516 CRC64;

O9K593 Length: 238 March 17, 2003 12:32 Type: P Check: 3282
Found using 'KTXS' (swope073.key)

...

102 EKTLPLQGMHSHLYKVPADOMENYANGYKKDEPVHVNNEILLGNAYGKTTSSDLRY
152
162 VOANMGOLKLDANAKMOQALTAHTGYFKSGEITODLMEPLPY

-----
1 match found in sequence:
g9k594; AmpC beta-lactamase (Fragment).
(from "lactxs_spt.pep")
TOIG of: g9k594 check: 3375 from: 1 to: 208

ID O9K594 PRELIMINARY; PRT; 208 AA.
AC O9K594;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE AmpC beta-lactamase (Fragment).
GN AMPC.
OS Hafnia alvei.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Hafnia.
OX NCBI_TaxID=569;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HAF Tn1.
RX MEDLINE=20291116; PubMed=10828397;
RA Nadjar D., Rouveau M., Verdet C., Donnay J.L., Herrmann J.L.,
Lagrange P.H., Philippou A., Arlet G.;
"Outbreak of Klebsiella pneumoniae producing transferable AmpC-type
RT beta-lactamase (ACC-1) originating from Hafnia alvei.";
RL FEMS Microbiol. Lett. 187:35-40(2000).
DR EMBL; AJ270940; CAB66896.1; -.
DR HSSP; P00811; 2BLS.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; beta-lactamase; 1.
FT NON_TER 208
SQ SEQUENCE 208 AA; 23020 MW; ED4B21863409C0FD CRC64;

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Q9K594 Length: 208 March 17, 2003 12:32 Type: P Check: 3375
Found using 'KTXS' (swope073.key)

92 EKTLLPOLGHHHSYLKVPADQMENTAMGYNKKDEPHVNMELTGNVATIKTSSDLLRY
142

152 VOANMGOLKLDANAKMQALATATHTGFRSGEITODLMEQLPY

1 match found in sequence:
q9k5k0 : Cefotaxime-hydrolyzing beta-lactamase (Fragment).
(from "lactxs_spt.pep")
TOIG of: q9k5k0 check: 7546 from: 1 to: 282

ID Q9K5K0 PRELIMINARY; PRT; 282 AA.
AC Q9K5K0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cefotaxime-hydrolyzing beta-lactamase (Fragment).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RA Minjun C., Yingshun X., Hui W.;
RT "Sequence of a novel cefotaxime-hydrolyzing beta-lactamase blaCTX-M-11."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY005110; AAF93177.1; -.
DR HSSP: Q47066; 1BZA.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase.A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTPAMASE.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 282
SQ SEQUENCE 282 AA; 30266 MW; 3ED1BF39D59C9022 CRC64;

Q9K5K0 Length: 282 March 17, 2003 12:32 Type: P Check: 7546
Found using 'KTXS' (swope073.key)

187 RAMAQLRLNLTLGKALGDSORAOVLVWKGNTTGASIQAGLPASVYVGDKTSGDYGIT
237

247 NDIAVWPKDRAPLIIVTYFTPOPKAESRRHYLAS

1 match found in sequence:
q9kgz1 : Choline binding protein E.
(from "lactxs_spt.pep")
TOIG of: q9kgz1 check: 4674 from: 1 to: 627

ID Q9KGZ1 PRELIMINARY; PRT; 627 AA.
AC Q9KGZ1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Choline binding protein E.
GN CBPE OR SP0930.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RA Gosink K.K., Rodgers M.E., Guglielmo C., Tuomanen E.I., Masure H.R.;
RT "The role of novel choline binding proteins in nasopharyngeal
colonization by Streptococcus pneumoniae";
RL Infect. Immun. 0:0-0(2000).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN-TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Uitterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae".
RL Science 293:498-506(2001).
DR EMBL: AF278687; AAF9769.1; -.
DR EMBL: AE007398; AAK75054.1; -.
DR TIGR: SP0930; -.
DR InterPro: IPR001279; Blactamase-like.
DR InterPro: IPR002479; CW_binding.
DR Pfam: PF01473; CW_binding; 9.
DR Pfam: PF00753; Lactamase_B; 1.
KW Complete proteome.
SQ SEQUENCE 627 AA; 72055 MW; EF3AA91F84B3CE17 CRC64;

Q9KGZ1 Length: 627 March 17, 2003 12:32 Type: P Check: 4674
Found using 'KTXS' (swope073.key)

520 AVGWIKDKRWYFLKENGQLVNGKTPGYVDSGGAWLVDSIEKSNITKTSHSEIKE
570

580 SKEVYKDLNKKETSQSHSVTNFTSODLTJSTSSSTSVNKS

1 match found in sequence:
q9kj90 : Beta-lactamase inhibitory protein BLIP-I precursor.
(from "lactxs_spt.pep")
TOIG of: q9kj90 check: 6086 from: 1 to: 186

ID Q9KJ90 PRELIMINARY; PRT; 186 AA.
AC Q9KJ90;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Beta-lactamase inhibitory protein BLIP-I precursor.
GN BLIA.
OS Streptomyces exfoliatus (Streptomyces hygroscopicus).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SMF19;
RX MEDLINE=20287557; PubMed=10747883;
RA Kang S.G., Park H.U., Lee H.S., Kim H.T., Lee K.J.;
RT "New beta-lactamase inhibitory protein (BLIP-I) from Streptomyces
exfoliatus SMF19 and its roles on the morphological differentiation";
RL J. Biol. Chem. 275:16851-16856(2000).
DR EMBL: AF201389; AAF74027.1; -.
FT CHAIN 30 186 BETA-LACTAMASE INHIBITORY PROTEIN BLIP-I.
SQ SEQUENCE 186 AA; 20087 MW; D19D0591FBD24AE3 CRC64;

09KJ90 Length: 186 March 17, 2003 12:32 Type: P Check: 6086
Found using 'KTXS' (swope073.key)

55 GGEACDPTGVIGDSILCFETESGDVAPYGGFPTDEGELMSKREXYLKAKTPSVLSTHY
105
115 NRTALGMEQAQMAAVPKDSCVSGESYENWPAKTGFEKYKYCA

1 match found in sequence:
g9kja7 : Class B carboxenemase Blab-8.
(from "lactixs_spt.pep")
TOIG of: g9kja7 check: 2192 from: 1 to: 248

ID 09KJA7 PRELIMINARY; PRT; 248 AA.
AC 09KJA7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
OS Class B carboxenemase Blab-8.
OC Flavobacterium meningosepticum.
OC Bacteria; CFB group; Flavobacteriia; Flavobacteriaceae;
OX NCBI_Taxid=238;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H01J100;
RX MEDLINE-20316804; PubMed-10858348;
RA Bellais S., Aubert D., Naas T., Nordmann P.;
RT "Molecular and biochemical heterogeneity of class B carboxenem-
hydrolyzing beta-lactamases in Chryseobacterium meningosepticum.";
RL Antimicrob. Agents Chemother. 44:1878-1886(2000).
DR EMBL; AF189305; AAF89161.1; -.
DR HSSP; P04190; 1BC2.
DR InterPro: IPR001018; Beta_lactamase_B.
DR InterPro: IPR001279; Blactamase-like.
DR Pfam; PF00753; lactamase_B; 1.
DR Prodom; PD007656; Beta_lactamase_B; 1.
DR PROSITE; PS00744; BETA_LACTAMASE_B_2; UNKNOWN_1.
SQ SEQUENCE 248 AA; 27961 MW; D340984EAD18059A CRC64;
09KJA7 Length: 248 March 17, 2003 12:32 Type: P Check: 2192
Found using 'KTXS' (swope073.key)

65 VIDSPMGEDKFKSFTDEIYKKGKKVIMNITATSHDDRAGLETFGLKAGTYSTKMTDS
115
125 ILAKENKPRAKYTFDNNKSFVKYKTEFOVYYPGKGHTADNVVWV
115
1 match found in sequence:
g9kja8 : Class B carboxenemase Blab-7.
(from "lactixs_spt.pep")
TOIG of: g9kja8 check: 2114 from: 1 to: 248
ID 09KJA8 PRELIMINARY; PRT; 248 AA.
AC 09KJA8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
OS Class B carboxenemase Blab-7.
OC Flavobacterium meningosepticum.

OC Bacteria; CFB group; Flavobacteriia; Flavobacteriaceae;
OC Chryseobacterium.
OX NCBI_Taxid=238;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ABI572;
RX MEDLINE-20316804; PubMed-10858348;
RA Bellais S., Aubert D., Naas T., Nordmann P.;
RT "Molecular and biochemical heterogeneity of class B carboxenem-
hydrolyzing beta-lactamases in Chryseobacterium meningosepticum.";
RL Antimicrob. Agents Chemother. 44:1878-1886(2000).
DR EMBL; AF189304; AAF89160.1; -.
DR HSSP; P04190; 1BC2.
DR InterPro: IPR001018; Beta_lactamase_B.
DR InterPro: IPR001279; Blactamase-like.
DR Pfam; PF00753; lactamase_B; 1.
DR Prodom; PD007656; Beta_lactamase_B; 1.
DR PROSITE; PS00744; BETA_LACTAMASE_B_2; UNKNOWN_1.
SQ SEQUENCE 248 AA; 27975 MW; C1DD1743CF858A9A CRC64;
09KJA8 Length: 248 March 17, 2003 12:32 Type: P Check: 2114
Found using 'KTXS' (swope073.key)

65 VIDSPMGEDKFKSFTDEIYKKGKKVIMNITATSHDDRAGLETFGLKAGTYSTKMTDS
115
125 ILAKENKPRAKYTFDNNKSFVKYKTEFOVYYPGKGHTADNVVWV
115

1 match found in sequence:
g9kja9 : Class B carboxenemase Blab-5.
(from "lactixs_spt.pep")
TOIG of: g9kja9 check: 4630 from: 1 to: 249

ID 09KJA9 PRELIMINARY; PRT; 249 AA.
AC 09KJA9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
OS Class B carboxenemase Blab-5.
OC Flavobacterium meningosepticum.
OC Bacteria; CFB group; Flavobacteriia; Flavobacteriaceae;
OC Chryseobacterium.
OX NCBI_Taxid=238;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CIP 79.5;
RX MEDLINE-20316804; PubMed-10858348;
RA Bellais S., Aubert D., Naas T., Nordmann P.;
RT "Molecular and biochemical heterogeneity of class B carboxenem-
hydrolyzing beta-lactamases in Chryseobacterium meningosepticum.";
RL Antimicrob. Agents Chemother. 44:1878-1886(2000).
DR EMBL; AF189303; AAF89159.1; -.
DR HSSP; P04190; 2BC2.
DR InterPro: IPR001018; Beta_lactamase_B.
DR InterPro: IPR001279; Blactamase-like.
DR Pfam; PF00753; lactamase_B; 1.
DR Prodom; PD007656; Beta_lactamase_B; 1.
DR PROSITE; PS00744; BETA_LACTAMASE_B_2; UNKNOWN_1.
SQ SEQUENCE 249 AA; 28161 MW; 252BA20FCCE1A837 CRC64;

09KJA9 Length: 249 March 17, 2003 12:32 Type: P Check: 4630
Found using 'KTXS' (swope073.key)

66 VIDSPMGEDKFKSFTDEIYKKGKKVIMNITATSHDDRAGLETFGLKAGTYSTKMTDS
115

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126 ILAKENKRAKYTFDNNKSEKVGNTFEQYVYVPGKGTADNVVW 116
...
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1 match found in sequence:
g9kj0 ; Class B carbapenemase Blab-6.
(from "laktxs_spt.pep")
TOIG of: g9kj0 check: 2327 from: 1 to: 248

ID 09KJB0 PRELIMINARY; PRT; 248 AA.
AC 09KJB0;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Class B carbapenemase Blab-6.
OS Flavobacterium meningosepticum.
OC Bacteria; CFB group; Flavobacteriia; Flavobacteriaceae;
OC Chryseobacterium.
OX NCBI_TaxID=238;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CIP 7830;
RX MEDLINE=20316804; PubMed=10958348;
RA Bellais S., Aubert D., Naas T., Nordmann P.;
RT "Molecular and biochemical heterogeneity of class B carbapenem-
RL hydrolyzing beta-lactamases in Chryseobacterium meningosepticum.";
DR Antimicrob. Agents Chemother. 44:1878-1886(2000).
DR EMBL; AF189302; AAF89158.1; -.
DR HSSP; P04190; 2BC2.
DR InterPro: IPR001018; Beta_lactamase_B.
DR InterPro: IPR001279; Blactamase-like.
DR Pfam; PF00753; Lactamase_B; 1.
DR PRODOM; PD007656; Beta_lactamase_B; 1.
DR PROSITE; PS00744; BETA_LACTAMASE_B_2; UNKNOWN_1.
SQ SEQUENCE 248 AA; 28046 MW; 720CF80F4A1EA837 CRC64;

09KJB0 length: 248 March 17, 2003 12:32 Type: P Check: 2327
Found using 'KTXS' (swope073.key)

...

65 VIDSPEWGDKEKSFTEDEYKKHGKVIAMNATSHDDRAGGLEFYFKLAKTSTKMTDS 115
ILAKENKRAKYTFDNNKSEKVGNTFEQYVYVPGKGTADNVVW

125 ILAKENKRAKYTFDNNKSEKVGNTFEQYVYVPGKGTADNVVW

...

2 matches found in sequence:
g9kj01 ; AMPC cephalosporinase precursor protein ACC-1d.
(from "laktxs_spt.pep")
TOIG of: g9kj01 check: 9677 from: 1 to: 390

ID 09KJD1 PRELIMINARY; PRT; 390 AA.
AC 09KJD1;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE AMPC cephalosporinase precursor protein ACC-1d.
GN ACC-1d.
OS Hafnia alvei.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX NCBI_TaxID=569;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HA-10;
RX MEDLINE=20277867; PubMed=10817695;
RA Girlich D., Naas T., Bellais S., Poirol L., Karim A., Nordmann P.;
RT "Biochemical-genetic characterization and regulation of expression of
RT an ACC-1-like chromosome-borne cephalosporinase from hafnia alvei.";
RL Antimicrob. Agents Chemother. 44:1470-1478(2000).
DR EMBL; AF180959; AAF86698.1; -.
DR HSSP; P00811; 1C3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Porin.
SQ SEQUENCE 390 AA; 42563 MW; C066094BEB2FE648 CRC64;

09KJD1 length: 390 March 17, 2003 12:32 Type: P Check: 9677
Found using 'KTXS' (swope073.key)

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RA Girlich D., Naas T., Bellais S., Poirol L., Karim A., Nordmann P.;
RT "Biochemical-genetic characterization and regulation of expression of
RT an ACC-1-like chromosome-borne cephalosporinase from hafnia alvei.";
RL Antimicrob. Agents Chemother. 44:1470-1478(2000).
DR EMBL; AF180961; AAF86700.1; -.
DR HSSP; P00811; 1C3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Porin.
SQ SEQUENCE 390 AA; 42563 MW; C066094BEB2FE648 CRC64;

09KJD1 length: 390 March 17, 2003 12:32 Type: P Check: 9677
Found using 'KTXS' (swope073.key)

...

201 EKTLLPQLGMHSHYLKVPADQENYAMGYNKKDEPVHVMELGNNAVGIKTTSSDLLRY 251
VOANNGQLKLDANAKMQALTAHTHTGYFKSGEITDLMEDLPYVSLPNLLTGNDAMAT

321 KSVATPIVPLPPQENWINKTSGNFGAYIAFPAKKMGIVMLANKNSIDORVTVAY 341
KILLSLEGNK

381 KILLSLEGNK

-----
2 matches found in sequence:
g9kj02 ; AMPC cephalosporinase precursor protein ACC-1c.
(from "laktxs_spt.pep")
TOIG of: g9kj02 check: 9641 from: 1 to: 390

ID 09KJD2 PRELIMINARY; PRT; 390 AA.
AC 09KJD2;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE AMPC cephalosporinase precursor protein ACC-1c.
GN ACC-1c.
OS Hafnia alvei.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX NCBI_TaxID=569;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HA-8;
RX MEDLINE=20277867; PubMed=10817695;
RA Girlich D., Naas T., Bellais S., Poirol L., Karim A., Nordmann P.;
RT "Biochemical-genetic characterization and regulation of expression of
RT an ACC-1-like chromosome-borne cephalosporinase from hafnia alvei.";
RL Antimicrob. Agents Chemother. 44:1470-1478(2000).
DR EMBL; AF180959; AAF86698.1; -.
DR HSSP; P00811; 1C3B.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Porin.
SQ SEQUENCE 390 AA; 42515 MW; 309BB887C4FE2432 CRC64;

09KJD2 length: 390 March 17, 2003 12:33 Type: P Check: 9641
Found using 'KTXS' (swope073.key)

...

201 EKTLLPQLGMHSHYLKVPADQENYAMGYNKKDEPVHVMELGNNAVGIKTTSSDLLRY 251

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261  VOANMGLKLDANAKMOALITATHTGYFKSGEITGLMEQLPYVSLPMLLTGNDMAMT
      |---|
321  KSVATPIVPLPPOENWINKTGSTNGFGAYIAFVPAKKMGIVMLANKNYSIDQRTVAY
      341
381  KILSLEGNK

-----
1 match found in sequence:
g9kj3d ; AMPC cephalosporinase protein ACC-3a (Fragment).
(from "lactxs_spt.pep")
TOIG of: g9kj3d check: 8151 from: 1 to: 377

ID  Q9KJ3D      PRELIMINARY;      PRT;      377 AA.
AC  Q9KJ3D;
DT  01-OCT-2000 (TREMBLrel. 15, Created)
DT  01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE  01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE  AMPC cephalosporinase protein ACC-3a (Fragment).
GN  ACC-3a.
OS  Hafnia alvei.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX  NCBI_TaxID=569;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=HA-5;
RX  MEDLINE=20277867; PubMed=10817695;
RA  Girlich D., Naas T., Bellais S., Poirel L., Karim A., Nordmann P.;
RT  "Biochemical genetic characterization and regulation of expression of
    an ACC-1-like chromosome-borne cephalosporinase from hafnia alvei.";
RL  Antimicrob. Agents Chemother. 44:1470-1478(2000).
DR  EMBL: AF180956; AAF86695.1;
DR  HSSP: P00811; 1C3B.
DR  InterPro: IPR001466; Beta_lactamase.
DR  InterPro: IPR001586; Beta_lactamase_C.
DR  Pfam: PF00144; beta-lactamase; 1.
DR  PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW  Porin.
FT  NON-TER
SQ  SEQUENCE 377 AA; 41256 MW; 050DB8FDECD9179F CRC64;

Q9KJ3D Length: 377 March 17, 2003 12:33 Type: P Check: 8151 ..
Found using 'KTXS' (swope073.key)

...

291  GKITODLMWEOQLPYVSLPDLTLTGNDMAMTKSVATPIVPLPPOENWINKTGSTNGFGA
      |---|
351  YIAFVPAKKMGIVMLANKNYSIDQRTV
      341

-----
2 matches found in sequence:
g9kj4d ; AMPC cephalosporinase precursor protein ACC-1b.
(from "lactxs_spt.pep")
TOIG of: g9kj4d check: 9401 from: 1 to: 390

ID  Q9KJ4D      PRELIMINARY;      PRT;      390 AA.
AC  Q9KJ4D;
DT  01-OCT-2000 (TREMBLrel. 15, Created)
DT  01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE  01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE  AMPC cephalosporinase precursor protein ACC-1b.
GN  ACC-1b.
OS  Hafnia alvei.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX  NCBI_TaxID=569;
RN  [1]
RP  SEQUENCE FROM N.A.

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RC  STRAIN=HA-4;
RX  MEDLINE=20277867; PubMed=10817695;
RA  Girlich D., Naas T., Bellais S., Poirel L., Karim A., Nordmann P.;
RT  "Biochemical genetic characterization and regulation of expression of
    an ACC-1-like chromosome-borne cephalosporinase from hafnia alvei.";
RL  Antimicrob. Agents Chemother. 44:1470-1478(2000).
DR  EMBL: AF180956; AAF86694.1;
DR  HSSP: P00811; 1C3B.
DR  InterPro: IPR001466; Beta_lactamase.
DR  InterPro: IPR001586; Beta_lactamase_C.
DR  Pfam: PF00144; beta-lactamase; 1.
DR  PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW  Porin.
SQ  SEQUENCE 390 AA; 42605 MW; C2DD604885DD7EPB CRC64;

Q9KJ4D Length: 390 March 17, 2003 12:33 Type: P Check: 9401 ..
Found using 'KTXS' (swope073.key)

...

201  EKITLPOLGMHSTYKVPADOMENYANGYKKDEPVHNMELIGNEAYGIKTSSDLRY
      |---|
261  VOANMGLKLDANAKMOALITATHTGYFKSGEITGLMEQLPYVSLPMLLTGNDMAMT
      251
321  KSVATPIVPLPPOENWINKTGSTNGFGAYIAFVPAKKMGIVMLANKNYSIDQRTVAY
      341
381  KILSLEGNK

-----
2 matches found in sequence:
g9kj5d ; AMPC cephalosporinase ACC-2.
(from "lactxs_spt.pep")
TOIG of: g9kj5d check: 64 from: 1 to: 390

ID  Q9KJ5D      PRELIMINARY;      PRT;      390 AA.
AC  Q9KJ5D;
DT  01-OCT-2000 (TREMBLrel. 15, Created)
DT  01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE  01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE  AMPC cephalosporinase ACC-2.
GN  ACC-2.
OS  Hafnia alvei.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX  NCBI_TaxID=569;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=HA-1;
RX  MEDLINE=20277867; PubMed=10817695;
RA  Girlich D., Naas T., Bellais S., Poirel L., Karim A., Nordmann P.;
RT  "Biochemical genetic characterization and regulation of expression of
    an ACC-1-like chromosome-borne cephalosporinase from hafnia alvei.";
RL  Antimicrob. Agents Chemother. 44:1470-1478(2000).
DR  EMBL: AF180952; AAF86691.1;
DR  HSSP: P00811; 1C3B.
DR  InterPro: IPR001466; Beta_lactamase.
DR  InterPro: IPR001586; Beta_lactamase_C.
DR  Pfam: PF00144; beta-lactamase; 1.
DR  PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW  Porin.
SQ  SEQUENCE 390 AA; 42631 MW; F77CA8B31C84CA09 CRC64;

Q9KJ5D Length: 390 March 17, 2003 12:33 Type: P Check: 64 ..
Found using 'KTXS' (swope073.key)

...

201  EQTILPLGMMNOTYKVPADOMENYANGYKKDEPVHNMELIGNEAYGIKTSSDLRY
      |---|

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251

261 VQANMGLKIDGNKAKIOHALTATHGTGFKSGEITODLMEQLPYVSLPMLTGNDMAFI

321 KSVATPIVPLPQENWINKTSTNGFGAYIAFVPAKKMIVMLANKNSIDQRTVAV
341

381 KILSSLEVNK

2 matches found in sequence:
g9k1j2 : AmpC-type class C beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: g9k1j2 check: 44 from: 1 to: 382

ID 09KJ12 PRELIMINARY; PRT; 382 AA.

AC 09KJ12;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE AmpC-type class C beta-lactamase.

GN CMT8.

OS Klebsiella pneumoniae.

OC Plasmid PKPW142.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Klebsiella.

OX NCBI_TaxID=573;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=KPM142;

RX MEDLINE=20277861; Pubmed=10817689;

RA Yan J.J., Wu S.M., Tsai S.H., Wu J.J., Su I.J.;

RT "Prevalence of SHV-12 among clinical isolates of Klebsiella pneumoniae
producing extended-spectrum beta-lactamases and identification of a
novel AmpC enzyme (CMT-8) in southern Taiwan."

RL Antimicrob. Agents Chemother. 44:1438-1442(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=KPM142;

RA Yan J.-J., Wu J.-J.;

RT "Nucleotide sequence analysis of a novel AmpC-type beta-lactamase,
CMT-8."

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF167990; AAD50818.2; -

DR HSSP: P05364; 2BLT.

DR InterPro: IPR001466; Beta_lactamase.

DR InterPro: IPR001586; Beta_lactamase_C.

DR Pfam: PF00144; beta-lactamase; 1.

DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.

KW Plasmid.

SQ SEQUENCE 382 AA; 40782 MW; BC424590FD0D4F82 CRC64;

09KJ12 Length: 382 March 17, 2003 12:33 Type: P Check: 44 ..

Found using 'KTXS' (swope073.key)

1 match found in sequence:
g9kvz4 : Beta-lactamase precursor.
(from "lactxs_spt.pep")
TOIG of: g9kvz4 check: 8936 from: 1 to: 274

ID 09KVZ4 PRELIMINARY; PRT; 274 AA.

AC 09KVZ4;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Beta-lactamase precursor.

GN OXA-23.

OS Acinetobacter baumannii.

OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;

OC Acinetobacter.

OX NCBI_TaxID=470;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RYC 52763/97;

(from "lactxs_spt.pep")
TOIG of: g9kw8 check: 461 from: 1 to: 752

ID 09KOW8 PRELIMINARY; PRT; 752 AA.

AC 09KOW8;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Rec2-related protein.

GN VC1879.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

OX NCBI_TaxID=666;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EL TOR N16961 / SEROTYPE O1;

RX MEDLINE=20406833; Pubmed=10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
Heidelberg J.F., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettein H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae."

RL Nature 406:477-483(2000).

DR EMBL: AE004263; AAF95027.1; -

DR TIGR: VC1879; -

DR InterPro: IPR001279; Blactamase-like.

DR InterPro: IPR004477; COMEC_N-term.

DR InterPro: IPR004797; COMEC_Rec2.

DR InterPro: IPR001950; TIF_S011.

DR Pfam: PF00753; lactamase_B; 1.

DR TIGRPFAM: TIGR00360; COMEC_N-term; 1.

DR TIGRPFAM: TIGR00361; COMEC_Rec2; 1.

DR PROSITE: PS01118; S011.1; UNKNOWN_1.

KW Complete proteome.

SQ SEQUENCE 752 AA; 85047 MW; A151745F42A0C462 CRC64;

09KOW8 Length: 752 March 17, 2003 12:33 Type: P Check: 461 ..

Found using 'KTXS' (swope073.key)

1 match found in sequence:
g9kvz4 : Beta-lactamase precursor.
(from "lactxs_spt.pep")
TOIG of: g9kvz4 check: 8936 from: 1 to: 274

ID 09KVZ4 PRELIMINARY; PRT; 274 AA.

AC 09KVZ4;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Beta-lactamase precursor.

GN OXA-23.

OS Acinetobacter baumannii.

OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;

OC Acinetobacter.

OX NCBI_TaxID=470;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RYC 52763/97;

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RX MEDLINE=20277880; PubMed=10817708;
RA Bou G., Oliver A., Martinez-Beltran J.;
RT "OXA-24, a novel class D beta-lactamase with carbapenemase activity in
an Acinetobacter baumannii clinical strain.";
RL Antimicrob Agents Chemother. 44:1556-1561(2000).
DR EMBL; AJ29129; CAB92323.1; -.
DR HSSP; P14489; 1E30.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 274 AA; 30810 MW; 5343DC532A8A4E6 CRC64;
O9KYZ4 Length: 274 March 17, 2003 12:33 Type: P Check: 8936
Found using 'KTxs' (swope073.key)

1 MKKFLIPFSISILVSLACSSIKTKSEDNFHISSQHEKAKITFDPAOTGVITIEG
1--1
24 27
61 KNLSTYGNALARANKEY

...

2 matches found in sequence:
q91387; Beta-lactamase class C.
(from "lactxs_spt.pep")
TOIG of: q91387 check: 7661 from: 1 to: 382

ID Q9L387 PRELIMINARY; PRT; 382 AA.
AC Q9L387;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Beta-lactamase class C.
GN FOX-4.
OS Escherichia coli.
OG Plasmid pcc-2.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GCE;
RX MEDLINE=20408594; PubMed=10952615;
RA Bou G., Oliver A., Ojeda M., Monzon C., Martinez-Beltran J.;
RT "Molecular characterization of FOX-4, a new AmpC-type plasmid-mediated
beta-lactamase from an Escherichia coli strain isolated in Spain.";
RL Antimicrob Agents Chemother. 44:2549-2553(2000).
DR EMBL; AJ277535; CAB89086.1; -.
DR HSSP; P05364; 2BLT.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Plasmid.
SQ SEQUENCE 382 AA; 40960 MW; 9476CE4C4A347A37 CRC64;
O9L387 Length: 382 March 17, 2003 12:33 Type: P Check: 7661
Found using 'KTxs' (swope073.key)

196 SQTLLPKLGLHHTYIQVPESAMANYAVGSKEDKPIRATPGVLAEAAGTKGSDADLLK
1--1
246
256 YEANNGYGDALAKSAIALHTGHSVGEWTOGLGWESYDYPTEQVLLAGNSPAVSFOA
316 NPVTRFAVPKAMGEORLYNKTGSGFGAYVAFVPAFGIALVMLANRNPPIEAVKAAHA
335
376 ILSQIAE

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2 matches found in sequence:
q913g2; Beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q913g2 check: 1561 from: 1 to: 382

ID Q9L3G2 PRELIMINARY; PRT; 382 AA.
AC Q9L3G2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Beta-lactamase.
GN BLA-MOX-2.
OS Klebsiella pneumoniae.
OG Plasmid pURB01.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KOL;
RA Raskine L., Borrel I., Sanson Le Pors M., Arlet G.;
RT "Characterization of MOX-2, an AmpC-type plasmid mediated beta-
lactamase from a clinical isolate of Klebsiella pneumoniae.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276453; CAB82578.1; -.
DR HSSP; P05364; 2BLT.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
KW Plasmid.
SQ SEQUENCE 382 AA; 41107 MW; C7364243B0DDADDA CRC64;
O9L3G2 Length: 382 March 17, 2003 12:33 Type: P Check: 1561
Found using 'KTxs' (swope073.key)

...

199 EQTLPLGLHHTYVNVPRQAMASVAYGSKEDKPIRVSPGMLADEAVGKITSADLLR
1--1
249
259 VKANISSVHDKALQQAISLTHKHGHSVGEWTOGLGWESYAVPYSEOTLLAGNSAKYLLA
319 NPTAAPREGSOMLFNKTGSGFGAYVAFVPAKGIGIVMLANRNPPIPARVKAHAHLLT
335
379 QLAR

2 matches found in sequence:
q913i5; Cephalosporinase.
(from "lactxs_spt.pep")
TOIG of: q913i5 check: 760 from: 1 to: 382

ID Q9L3I5 PRELIMINARY; PRT; 382 AA.
AC Q9L3I5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cephalosporinase.
GN CEPH.
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
OC Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T429125;
RX MEDLINE=20517399; PubMed=11062187;

```

RA Avison M.B., Niumsup P., Walsh T.R., Bennett P.M.;
 RT "Aeromonas hydrophila Amp^r and Cep^r beta-lactamases: derepressed
 expression in mutants of *Escherichia coli* lacking creB.";
 RL J. Antimicrob. Chemother. 46:695-702(2000).
 DR EMBL: AJ276030; CAB76925.1; -.
 DR HSSP: P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Porin.
 SQ SEQUENCE 382 AA; 40701 MW; A8710D3204C6A666 CRC64;

Q9L3V7 Length: 382 March 17, 2003 12:33 Type: P Check: 760
 Found using 'ktxs' (swope073.key)

196 EQTLPGHHTHYLDVPEAAMASVAYGYSKEDKPIRVNPGMLADEAYGKTSADLLAF
 246

256 VKANISGVDDKALQQAISLTGQGRYSVGEEMTGIGWESYTPVSEQTLLAGNSAVIYNA

316 NPVKFVAASQETGARGLNKKTSGNGGAYVAFYPAKGIGIVMLANRNPENRISAAHA
 335

376 ILSQLAP

 1 match found in sequence:
 q9L3V7: Class C beta-lactamase.
 (from "lactxs_spt.pep")

TOIG of: q9L3V7 check: 1841 from: 1 to: 378

ID Q9L3V7 PRELIMINARY; PRT; 378 AA.
 AC Q9L3V7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Class C beta-lactamase.
 GN AMPC.
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 OX NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SL573;
 RA Barnaud G., Arlet G.J., Labia R., Philippot A.;
 RT "Nucleotide sequence of ampC gene of *Serratia marcescens* and its
 regulatory gene ampr.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ271368; CAB69829.1; -.
 DR HSSP: P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 378 AA; 41250 MW; 7B1FBA206A5C35AD CRC64;

Q9L3V7 Length: 378 March 17, 2003 12:33 Type: P Check: 1841
 Found using 'ktxs' (swope073.key)

280 FTODLWENYEPYVKLSRLVEGNAGIMNGTPTATITPPQPELRAGMYNKTSGTGFSR
 330

340 YAVFIPAKNIADVMLANKMFPNDREAVAHIIQALEKH

 1 match found in sequence:
 q9L4R5: Beta-lactamase class C (EC 3.5.2.6).
 (from "lactxs_spt.pep")
 TOIG of: q9L4R5 check: 8099 from: 1 to: 383

ID Q9L4R5 PRELIMINARY; PRT; 383 AA.
 AC Q9L4R5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-lactamase class C (EC 3.5.2.6).
 GN AMPC.
 OS Acinetobacter baumannii.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acinetobacter.
 OX NCBI_TaxID=470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RYC 52763/97;
 RX MEDLINE=20106996; PubMed=10639377;
 RA Bou G., Martinez-Beltran J.;
 RT "Cloning, Nucleotide Sequencing, and Analysis of the Gene Encoding an
 AmpC beta-lactamase in *Acinetobacter baumannii*.";
 RL Antimicrob. Agents Chemother. 44:428-432(2000).
 DR EMBL: AJ009979; CAB77444.1; -.
 DR HSSP: P00811; 1C3B.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 KW Hydrolase.
 SQ SEQUENCE 383 AA; 43208 MW; 1F53056E55AF6D18 CRC64;

Q9L4R5 Length: 383 March 17, 2003 12:33 Type: P Check: 8099
 Found using 'ktxs' (swope073.key)

286 VNTMYALGMEHSTYATITQTLDSNSQIYVKKPNKYTAISKEPSVKMHNKGTNRFGT
 336

346 YVVFIPKENGIVMLNKRIPNEERIKAYAVLVNLIK

 1 match found in sequence:
 q9L587: Cefotaxime-hydrolyzing beta-lactamase (Fragment).
 (from "lactxs_spt.pep")
 TOIG of: q9L587 check: 915 from: 1 to: 291

ID Q9L587 PRELIMINARY; PRT; 291 AA.
 AC Q9L587;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Cefotaxime-hydrolyzing beta-lactamase (Fragment).
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21091843; PubMed=11158766;
 RA Oliver A., Perez-Diaz J.C., Coque T.M., Baguerio F., Canton R.;
 RT "Nucleotide Sequence and Characterization of a Novel Cefotaxime-
 Hydrolyzing beta-lactamase (CTX-M-10) Isolated in Spain.";
 RL Antimicrob. Agents Chemother. 45:616-620(2001).
 DR EMBL: AF255298; AAF65843.1; -.
 DR HSSP: Q47066; 1BZA.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.

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DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 291
SQ SEQUENCE 291 AA; 31201 MW; 43FBESCAG656FBA4 CRC64;

Q91567 Length: 291 March 17, 2003 12:33 Type: P Check: 915
Found using 'KTXS' (swope073.key)

...

187 RAMAOTLRNLGLKALGDSQRAQLVTWKGNTTGAASIQAGLPASWVYGDGTGSDYGT
|---|
237

247 NDIAVIMPGRAPLVLTFTYTPQPNASRRDVLASAKIYTDG

...

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1 match found in sequence:
Q91567 ; Beta-lactamase CTX-M-15.
(from "lactxs_spt.pep")
TOIG of: q91567 check: 9380 from: 1 to: 291

ID Q91566 PRELIMINARY; PRT; 291 AA.
AC Q91566;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Beta-lactamase CTX-M-15.
GN BLACTX-M-15.
OS Klebsiella pneumoniae.
OC Bacteri; gamma subdivision; Enterobacteriaceae;
OC Bacteri; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ACH17;
RA Chanawong A., W'zali F.H., Heritage J., Xiong J.-H., Hawkey P.M.;
RT "Dissemination and evolution of new, plasmid-mediated extended-
RT spectrum beta-lactamases (CTX-M-13, CTX-M-14 and CTX-M-15) and
RT prevalence of SHV-12 among Enterobacteriaceae isolated from Guangzhou,
RT People's Republic of China."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252623; AAF72531.1; -
DR HSSP: Q47066; 1BZA.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 291 AA; 31126 MW; C06BFEE2A5FCC4 CRC64;

Q91566 Length: 291 March 17, 2003 12:33 Type: P Check: 9380
Found using 'KTXS' (swope073.key)

...

187 RAMAOTLRNLGLKALGDSQRAQLVTWKGNTTGAASIRAGLPTSWTVGDKTSGDYGT
|---|
237

247 NDIAVIMPGRAPLVLTFTYTPQPNASRRDVLASAKIYTDG

...

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1 match found in sequence:
Q91567 ; CTX-M-like-beta-lactamase (TOHO-2 like beta-lactamase) (CTX-M-14
(from "lactxs_spt.pep")
TOIG of: q91567 check: 8702 from: 1 to: 291

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ID Q915C7 PRELIMINARY; PRT; 291 AA.
AC Q915C7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CTX-M-like-beta-lactamase (TOHO-2 like beta-lactamase) (CTX-M-14
DE beta-lactamase) (Cefotaxime-hydrolyzing beta-lactamase CTX-M-18)
DE (Class A beta-lactamase).
GN BLA00E-2 OR BLACTX-M-14 OR BLAT0HO-3.
OS Escherichia coli, and
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 573;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=ACH13;
RA Chanawong A., W'zali F.H., Heritage J., Xiong J.-H., Hawkey P.M.;
RT "Dissemination and evolution of new, plasmid-mediated extended-
RT spectrum beta-lactamases among Enterobacteriaceae isolates from the
RT People's Republic of China."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RA Muratani T., Kobayashi T., Nagasaki M., Takahashi K., Matsumoto T.;
RT "Prevalence of ODE-2 a TOHO-2 like novel beta-lactamase producing
RT Escherichia coli in Fukuoka, Japan."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=TN02;
RA Saladin M., Bao Cao V.T., Lambert T., Donay J.L., Herrmann J.L.,
RA Ould Hocine Z., Verdet C., Delisle F., Philippot A., Arlet G.;
RT "Diversity of CTX-M beta-lactamases and their promoter regions from
RT enterobacteriaceae isolated in three hospitals of downtown Paris."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=K.pneumoniae;
RA Poirel L., Naas T., Le Thomas I., Karim A., Bingen E., Nordmann P.;
RT "CTX-M-type extended-spectrum beta-lactamase that hydrolyzes
RT ceftazidime through a single amino acid substitution in the omega
RT loop."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; PLASMID=PMY1102;
RA Ishii Y., Galleni M., Ma L., Keizo Y., Frere J.;
RT "Cloning and sequencing of the gene encoding class A beta-lactamase."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252622; AAF72530.1; -
DR EMBL: AF311345; AAG47784.1; -
DR EMBL: AJ416341; CAC95170.1; -
DR EMBL: AF325133; AAK55533.1; -
DR EMBL: AB038771; BAB62310.1; -
DR HSSP: Q47066; 1BZA.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 291 AA; 30979 MW; C8DCID77EAE469E CRC64;

Q915C7 Length: 291 March 17, 2003 12:33 Type: P Check: 8702
Found using 'KTXS' (swope073.key)

...

187 RAMAOTLRNLGLKALGDSQRAQLVTWKGNTTGAASIRAGLPTSWTVGDKTSGDYGT
|---|

```

237

247 NDIAVIMPOGRAPLVLYTFYTPQONASRRDVLASARIITAE

1 match found in sequence:
 q915c8 ; CTX-M-like-beta-lactamase (TOHO-like beta-lactamase) (CTX-M-9 like
 (from "lacktxs_spt.pep")
 TOIG of: q915c8 check: 8576 from: 1 to: 291

ID Q915C8 PRELIMINARY; PRT; 291 AA.
 AC Q915C8; Q9PR34; 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE CTX-M-like-beta-lactamase (TOHO-like beta-lactamase) (CTX-M-9 like
 beta-lactamase).
 GN BLACTX-M-9 LIKE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NC NCBL_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ACH08;
 RA Chanawong A., M'zali F.H., Heritage J., Xiong J.-H., Hawkey P.M.;
 RT "Dissemination and evolution of new, plasmid-mediated extended-
 RT spectrum beta-lactamases among Enterobacteriaceae isolates from the
 RT People's Republic of China";
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-785-D;
 RX MEDLINE=20316819; PubMed=10858363;
 RA Sebaste M., Tarrago R., Navarro F., Miro E., Verges C., Barbe J.,
 RA Prats G.;
 RT "Cloning and sequence of the gene encoding a novel cefotaxime-
 RT hydrolyzing beta-lactamase (CTX-M-9) from Escherichia coli in Spain.";
 RL Anticrib. Agents Chemother. 44:1970-1973(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RAJ;
 RA Saladin M., Bao Cao V.T., Lambert T., Donay J.L., Herrmann J.L.,
 RA Ould Hocine Z., Verdier C., Delisle F., Philippot A., Arlet G.;
 RT "Diversity of CTX-M beta-lactamases and their promoter regions from
 RT enterobacteriaceae isolated in three hospitals of downtown Paris.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF252621; AAF72529.1; -;
 DR EMBL: AF174129; AAF05311.2; -;
 DR EMBL: A416345; CAC95176.1; -;
 DR HSSP; Q47066; IBZA.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase.A.
 DR Pfam: PF00144; beta-lactamase.1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE.A.1.
 SQ SEQUENCE 291 AA; 30951 MW; C8CB0A7739B9469E CRC64;

Q915C8 Length: 291 March 17, 2003 12:33 Type: P Check: 8576
 Found using 'KTXS' (swope073.key)

187 RAMAQLRLQLTLGHALGETORALVTLWKNTGTAASIRAGLFTSWTAGCKTSGDYCTT
 237

247 NDIAVIMPOGRAPLVLYTFYTPQONASRRDVLASARIITAE

...

1 match found in sequence:
 q91rw8 ; Hydrolase-like protein.
 (from "lacktxs_spt.pep")
 TOIG of: q91rw8 check: 9029 from: 1 to: 309

ID Q91RW8 PRELIMINARY; PRT; 309 AA.
 AC Q91RW8;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Hydrolase-like protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids. II; Brassicales; Brassicaceae; Arabidopsis.
 GN NCBL_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty p1 and TAC
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 DR EMBL: AB028610; BAB02903.1; -;
 DR InterPro: IPR001279; Lactamase-like.
 DR Pfam: PF00753; lactamase.B.1.
 SQ SEQUENCE 309 AA; 34710 MW; 73DE9B332FED214A CRC64;

Q91RW8 Length: 309 March 17, 2003 12:33 Type: P Check: 9029
 Found using 'KTXS' (swope073.key)

1 MEDYCCVLLDSANGDALVSSDSSSEIVFMGTGNSGICLPVSLPLKTSVCTKATE
 50 53

61 PCGNRRRLNTSILVYIRPSTGNTLIDCKEFTYHSALRWPPPT

1 match found in sequence:
 q9pm86 ; Hypothetical protein Cj1589.
 (from "lacktxs_spt.pep")
 TOIG of: q9pm86 check: 8253 from: 1 to: 265

ID Q9PM86 PRELIMINARY; PRT; 265 AA.
 AC Q9PM86;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Hypothetical protein Cj1589.
 GN Cj1589.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 OC Campylobacter.
 GN NCBL_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NCCTC 11168;
 RX MEDLINE=20150912; PubMed=10688204;
 RA Parkhill J., Wren B.W., Mungall K., Kelley J.M., Churcher C.,
 RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,
 RA Jagers K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrett B.G.;

RT "The genome sequence of the food-borne pathogen *Campylobacter jejuni*
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000)
DR EMBL: AL139079; CAB73577.1; -
DR InterPro: IPR001279; B1actamase-like.
DR Pfam: PF00753; Lactamase-B; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 265 AA; 31015 MW; 6928648765700B58 CRC64;

Q9PM86 Length: 265 March 17, 2003 12:33 Type: P Check: 8253
Found using 'KTXS' (swope073.key)

1 MFNFITLLKTNLFLEKTSKNSNQTHIISLKQSDDEFNLFLFSFLVPSDEDEKNFIE
19 22

61 KTKTKIKRNEHN

1 match found in sequence:
q9raz8 : CME-2 extended spectrum beta-lactamase.
(from "lactxs_spt.pep")
TOIG of: q9raz8 check: 6709 from: 1 to: 297

ID Q9RAZ8 PRELIMINARY; PRT; 297 AA.
AC Q9RAZ8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE CME-2 extended spectrum beta-lactamase.
OS Flavobacterium meningosepticum.
OC Bacteria; CFB group; Flavobacteriia; Flavobacteriaceae;
OX NCBI_TaxID=238;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PINT;
RX MEDLINE=20068667; PubMed=10602714;
RA Bellais S., Polrel L., Naas T., Girlich D., Nordmann P.;
RT "Genetic-biochemical analysis and distribution of the Ambler class A
beta-lactamase CME-2, responsible for extended-spectrum cephalosporin
RT resistance in *Chryseobacterium* (Flavobacterium) meningosepticum.";
RL Antimicrob. Agents Chemother. 44:1-9(2000).
DR EMBL: AF033200; AAP19261.1; -
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; Beta-lactamase; 1.
SQ SEQUENCE 297 AA; 32983 MW; 568D3230F10ZE0B3 CRC64;

Q9RAZ8 Length: 297 March 17, 2003 12:33 Type: P Check: 6709
Found using 'KTXS' (swope073.key)

181 TASAVKTLKAFYKGFSLKSRSTIFLMDIMTKNTGMSKLPGLLPKVMARKTSSGSKMKN
231

241 GLTIANDSGIVTLANGKHVAIAVFKDSMESEVNCGIIAQS

1 match found in sequence:

q9raz9 : CME-1 protein precursor.
(from "lactxs_spt.pep")
TOIG of: q9raz9 check: 4578 from: 1 to: 295

ID Q9RAZ9 PRELIMINARY; PRT; 295 AA.
AC Q9RAZ9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE CME-1 protein precursor.
GN BLAAME.
OS Flavobacterium meningosepticum.
OC Bacteria; CFB group; Flavobacteriia; Flavobacteriaceae;
OX NCBI_TaxID=238;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CCUG4310;
RX MEDLINE=99402676; PubMed=10471563;
RA Rossolini G.M., Franceschini N., Caravelli B., Roccio M.L.,
RA Gallen I.M., Frere J.M., Amicosante G.;
RT "Cloning of a *Chryseobacterium* (Flavobacterium) meningosepticum
RT chromosomal gene (blaCME) encoding an extended-spectrum class A beta-
RT lactamase related to the Bacteroides cephalosporinases and the YEB-1
RT and PER beta-lactamases.";
RL Antimicrob. Agents Chemother. 43:2193-2199(1999).
DR EMBL: AJ006275; CAB55427.1; -
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; Beta_lactamase; 1.
KW Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 295 CME-1 PROTEIN.
SQ SEQUENCE 295 AA; 32804 MW; 4EFD31148C6DF6AC CRC64;

Q9RAZ9 Length: 295 March 17, 2003 12:33 Type: P Check: 4578
Found using 'KTXS' (swope073.key)

161 TASAVKTLKAFYKGFSLKSRSTIFLMDIMTKNTGMSKLPGLLPKVMARKTSSGSKMKN
231

241 GLTIANDSGIVTLANGKHVAIAVFKDSMESEVNCGIIAQS

1 match found in sequence:
q9rb01 : Beta-lactamase BLAB2 (Class B CARBAPENEMASE BLAB-2).
(from "lactxs_spt.pep")
TOIG of: q9rb01 check: 3770 from: 1 to: 249

ID Q9RB01 PRELIMINARY; PRT; 249 AA.
AC Q9RB01;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Beta-lactamase BLAB2 (Class B CARBAPENEMASE BLAB-2).
GN BLAB2.
OS Flavobacterium meningosepticum.
OC Bacteria; CFB group; Flavobacteriia; Flavobacteriaceae;
OX NCBI_TaxID=238;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97/P/5448;
RX MEDLINE=20316804; PubMed=10858348;
RA Bellais S., Audert D., Naas T., Nordmann P.;
RT "Molecular and biochemical heterogeneity of class B carbapenem-
RT hydrolyzing beta-lactamases in *Chryseobacterium meningosepticum*,";
RL Antimicrob. Agents Chemother. 44:1878-1886(2000).
DR EMBL: AF126542; AAD43145.1; -

DR EMBL: AF189300; AAP89156.1; -.
 DR HSSP: P04190; IBC2.
 DR InterPro: IPR001018; Beta_lactamase_B.
 DR InterPro: IPR001279; Bactamase-like.
 DR Pfam: PF00753; Lactamase_B; 1.
 DR ProDom: PD007656; Beta_lactamase_B; 1.
 DR PROSITE: PS00744; BETA_LACTAMASE_B_2; 1.
 SQ SEQUENCE 249 AA: 28149 MW: FE6050F18DE898E6 CRC64;

09RB01 Length: 249 March 17, 2003 12:33 Type: P Check: 3770
 Found using 'KTXS' (swope073.key)

66 VIDCPGCEDEKFSPTDEIYKRGKVMYIMNIATHSHDDRAGLEFYGKIGAKYISTMTDS
 116

126 ILAKENKPRQYTFDNKSKFYVKSSEFYVYPPGKHGTADNVVYM

1 match found in sequence:
 q9rbq0 : L2 beta-lactamase precursor.
 (from "lactxs_spt.pep")
 TOIG of: q9rbq0 check: 6127 from: 1 to: 303

ID 09RB00 PRELIMINARY; PRT; 303 AA.
 AC 09RB00;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE L2 beta-lactamase precursor.
 GN BLAL2.
 OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Stenotrophomonas.
 OX NCBI_TaxID=40324;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J675A;
 RC MEDLINE=21091811; PubMed=11158734;
 RA Avison M.B., Higgins C.S., von Heldreich C.J., Bennett P.M.,
 RA Walsh T.R.;
 RT "Plasmid location and molecular heterogeneity of the L1 and L2 beta-lactamase genes from Stenotrophomonas maltophilia."
 RL Antimicrob. Agents Chemother. 45:413-419(2001).
 DR EMBL: AJ251817; CAB63491.1; -.
 DR HSSP: Q47066; 1BZA.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 KW signal.
 FT SIGNAL 1 21
 FT CHAIN 22 303 L2 BETA-LACTAMASE.
 SQ SEQUENCE 303 AA: 32020 MW: 536CF9A5021EE1F0 CRC64;

09RB00 Length: 303 March 17, 2003 12:33 Type: P Check: 6127
 Found using 'KTXS' (swope073.key)

197 GAMATLQRVVLGEVLPASRQQLADWLIDNETGDACLRAGLGKRMVGDXTGSGEDAR
 247

257 NDIATLMPVAGAPVWLTAYLQAGALSYEQRSVLAQVGRADR

1 match found in sequence:
 q9rbq1 : L2 beta-lactamase precursor.
 (from "lactxs_spt.pep")
 TOIG of: q9rbq1 check: 2942 from: 1 to: 303

ID 09RB01 PRELIMINARY; PRT; 303 AA.
 AC 09RB01;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE L2 beta-lactamase precursor.
 GN BLAL2.
 OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Stenotrophomonas.
 OX NCBI_TaxID=40324;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K279A;
 RC MEDLINE=21091811; PubMed=11158734;
 RA Avison M.B., Higgins C.S., von Heldreich C.J., Bennett P.M.,
 RA Walsh T.R.;
 RT "Plasmid location and molecular heterogeneity of the L1 and L2 beta-lactamase genes from Stenotrophomonas maltophilia."
 RL Antimicrob. Agents Chemother. 45:413-419(2001).
 DR EMBL: AJ251816; CAB63490.1; -.
 DR HSSP: Q47066; 1BZA.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 KW signal.
 FT SIGNAL 1 21
 FT CHAIN 22 303 L2 BETA-LACTAMASE.
 SQ SEQUENCE 303 AA: 31998 MW: BEFD3717C680DB73 CRC64;

09RB01 Length: 303 March 17, 2003 12:33 Type: P Check: 2942
 Found using 'KTXS' (swope073.key)

197 AAMATLQRVVLGEVLPASRQQLADWLIDNETGDACLRAGLGKRMVGDXTGSGEDAR
 247

257 NDIATLMPVAGAPVWLTAYLQAGALSYEQRSVLAQVGRADR

1 match found in sequence:
 q9rer5 : Beta-lactamase AmpC.
 (from "lactxs_spt.pep")
 TOIG of: q9rer5 check: 1524 from: 1 to: 381

ID 09RER5 PRELIMINARY; PRT; 381 AA.
 AC 09RER5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE beta-lactamase AmpC.
 GN AMPC.
 OS Enterobacter aerogenes (Aerobacter aerogenes).
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=548;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20493130; PubMed=11036041;

RA Preston K.E., Radomski C.C.A., Venezia R.A.;
 RT "Nucleotide Sequence of the Chromosomal ampC Gene of Enterobacter
 aerogenes.";
 RL Antimicrob. Agents Chemother. 44:3158-3162(2000).
 DR EMBL: AF211348; AAF18992.1; -.
 DR HSSP: P05364; 2BLT.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR001586; Beta_lactamase_C.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PROSITE: PS00336; BETA_LACTAMASE_C; 1.
 SQ SEQUENCE 381 AA; 41601 MW; FA7BF5B8B206C80 CRC64;

Q9RI05 Length: 381 March 17, 2003 12:33 Type: P Check: 1524
 Found using 'KTXS' (swope073.key)

285 MYGLGEMINMPFPAEVVINSNDKVALAAPTAVNPAPSVKAWHKTGTSGTGGFS
 335

345 YVAFIPQDGLIVLANKSVNPERVKAHYHLEALQ

1 match found in sequence:
 q9ri06 ; Beta-lactamase FONA-6.
 (from "lactxs_spt.pep")
 TOIG of: q9ri06 check: 3543 from: 1 to: 295

ID Q9RI06 PRELIMINARY; PRT; 295 AA.
 AC Q9RI06;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Beta-lactamase FONA-6.
 GN FONA-6.
 OS Serratia fonticola.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 OX NCBI_TaxID=47917;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF18;
 RA Humenik C., Arlet G., Labia R., Philippou A.;
 RT "Beta-lactamases of Serratia fonticola: susceptibility patterns,
 overproduction and genetic approach.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ251244; CAB61643.1; -.
 DR HSSP: Q47066; 1BZA.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 SQ SEQUENCE 295 AA; 31862 MW; EB54F6E9DDEBC87 CRC64;

Q9RI06 Length: 295 March 17, 2003 12:33 Type: P Check: 3543
 Found using 'KTXS' (swope073.key)

191 LMAKSLQNLTLGKALGPORAQLVEMWKGNTTGASIRAGLPTTWVVGDTGSGDYGT
 241

251 NDIAVIMPANHAPLVIVTYFTQPOQNAERKRDVLAATAKIYTEG

1 match found in sequence:
 q9ri08 ; Beta-lactamase FONA-5.
 (from "lactxs_spt.pep")
 TOIG of: q9ri08 check: 3117 from: 1 to: 295

ID Q9RI08 PRELIMINARY; PRT; 295 AA.
 AC Q9RI08;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Beta-lactamase FONA-5.
 GN FONA-5.
 OS Serratia fonticola.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 OX NCBI_TaxID=47917;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF17;
 RA Humenik C., Arlet G., Labia R., Philippou A.;
 RT "Beta-lactamases of Serratia fonticola: susceptibility patterns,
 overproduction and genetic approach.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ251243; CAB61643.1; -.
 DR HSSP: Q47066; 1BZA.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 SQ SEQUENCE 295 AA; 31913 MW; 245F9A496E990708 CRC64;

Q9RI08 Length: 295 March 17, 2003 12:33 Type: P Check: 3117
 Found using 'KTXS' (swope073.key)

191 QAMAISLQNLTLGKALGPORAQLVEMWKGNTTGASIRAGLPTTWVVGDTGSGDYGT
 241

251 NDIAVIMPANHAPLVIVTYFTQPOQNAERKRDVLAATAKIYTEG

1 match found in sequence:
 q9ri0 ; Beta-lactamase FONA-4.
 (from "lactxs_spt.pep")
 TOIG of: q9ri0 check: 3355 from: 1 to: 295

ID Q9RI0 PRELIMINARY; PRT; 295 AA.
 AC Q9RI0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Beta-lactamase FONA-4.
 GN FONA-4.
 OS Serratia fonticola.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 OX NCBI_TaxID=47917;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF15;
 RA Humenik C., Arlet G., Labia R., Philippou A.;
 RT "Beta-lactamases of Serratia fonticola: susceptibility patterns,
 overproduction and genetic approach.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ251242; CAB61641.1; -.
 DR HSSP: Q47066; 1BZA.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 SQ SEQUENCE 295 AA; 31849 MW; 43CF96C8E98509AF CRC64;

Q9RI0 Length: 295 March 17, 2003 12:33 Type: P Check: 3355

Found using 'KTXS' (swope073.key)

191 LAMAKSLQNLTLGKALGEPQRAQLVEMMKNTTGASIRAGLPTTWIVGDKTSGSDYGT

1--1
241

251 NDIIVIPANHAPLVLTFTPTPOQNAEARKDVLAAAKIVTEG

1 match found in sequence:
q9rir1 ; Beta-lactamase FON-3.
(from "lacktxs_spt.pep")

TOIG of: q9rir1 check: 3543 from: 1 to: 295

ID O9RIR1 PRELIMINARY; PRT; 295 AA.
AC O9RIR1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Beta-lactamase FON-3.
GN FON-3.
OS Serratia fonticola.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=47917;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SF13;
RA Humeniuk C., Arlet G., Labia R., Philippou A.;
RT "Beta-lactamases of Serratia fonticola: susceptibility patterns, overproduction and genetic approach.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251241; CAB61639.1; -
DR HSSP; Q47066; 1BZA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
SQ SEQUENCE 295 AA; 31917 MW; 3C86B9AC918DD623 CRC64;
O9RIR1 Length: 295 March 17, 2003 12:33 Type: P Check: 3543
Found using 'KTXS' (swope073.key)

191 LAMAKSLQNLTLGKALGEPQRAQLVEMMKNTTGASIRAGLPTTWIVGDKTSGSDYGT

1--1
241

251 NDIIVIPANHAPLVLTFTPTPOQNAEARKDVLAAAKIVTEG

1 match found in sequence:
q9rir2 ; Class A beta-lactamase FON-2.
(from "lacktxs_spt.pep")

TOIG of: q9rir2 check: 3527 from: 1 to: 295

ID O9RIR2 PRELIMINARY; PRT; 295 AA.
AC O9RIR2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Class A beta-lactamase FON-2.
GN FON-2.
OS Serratia fonticola.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.

OX NCBI_TaxID=47917;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-SF13;

RA Humeniuk C., Arlet G., Labia R., Philippou A.;

RT "Beta-lactamases of Serratia fonticola: susceptibility patterns, overproduction and genetic approach.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ251240; CAB61637.1; -

DR HSSP; Q47066; 1BZA.

DR InterPro; IPR001466; Beta_lactamase.

DR InterPro; IPR000871; Beta_lactamase_A.

DR Pfam; PF00144; beta-lactamase; 1.

DR PRINTS; PR00118; BLACTAMASEA.

SQ SEQUENCE 295 AA; 31874 MW; 5E5051C92560389A CRC64;

O9RIR2 Length: 295 March 17, 2003 12:33 Type: P Check: 3527
Found using 'KTXS' (swope073.key)

191 LAMAKSLQNLTLGKALGEPQRAQLVEMMKNTTGASIRAGLPTTWIVGDKTSGSDYGT

1--1
241

251 NDIIVIPANHAPLVLTFTPTPOQNAEARKDVLAAAKIVTEG

1 match found in sequence:
q9rir3 ; Class A beta-lactamase FON-1.
(from "lacktxs_spt.pep")

TOIG of: q9rir3 check: 3329 from: 1 to: 295

ID O9RIR3 PRELIMINARY; PRT; 295 AA.
AC O9RIR3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Class A beta-lactamase FON-1.
GN FON-1.
OS Serratia fonticola.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=47917;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CIF78.64T;
RA Humeniuk C., Arlet G., Labia R., Philippou A.;
RT "Beta-lactamases of Serratia fonticola: susceptibility patterns, overproduction and genetic approach.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251239; CAB61635.1; -
DR HSSP; Q47066; 1BZA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
SQ SEQUENCE 295 AA; 31863 MW; 6FDEB507DB51BAF9 CRC64;

O9RIR3 Length: 295 March 17, 2003 12:33 Type: P Check: 3329
Found using 'KTXS' (swope073.key)

191 LAMAKSLQNLTLGKALGEPQRAQLVEMMKNTTGASIRAGLPTTWIVGDKTSGSDYGT

1--1
241

251 NDIIVIPANHAPLVLTFTPTPOQNAEARKDVLAAAKIVTEG

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1 match found in sequence:
q9rlx4 : Beta-lactamase class A.
(from "lactxs_spt.pep")
TOIG of: q9rlx4 check: 8226 from: 1 to: 291

ID 09RLX4 PRELIMINARY; PRT; 291 AA.
AC 09RLX4;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Beta-lactamase class A.
GN KLUA-1 OR KLUA-12 OR KLUA-3 OR KLUA-4.
OS Kluvera ascorbata.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Kluvera.
OX NCBI_TaxID=51288;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CIP82.95T;
RA Humenik C., Arlet G., Labia R., Philippou A.;
RT "Beta-lactamase of Kluvera ascorbata: progenitor of some plasmid-
RT encoded CTX-M types."
DR EMBL: AJ272538; CAB59824.1; -
DR EMBL: AJ427469; CAD20593.1; -
DR EMBL: AJ427461; CAD20585.1; -
DR EMBL: AJ427462; CAD20586.1; -
DR HSSP: Q47066; 1BZA.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase_1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 291 AA; 31377 MW; 9B0FDEAD5E2E7C0 CRC64;

09RLX4 Length: 291 March 17, 2003 12:33 Type: P Check: 8226
Found using 'KTXS' (swope073.key)

187 LAMAQTLNLTGKALAEQRAQLVTLKGNLTGSASIRAGLPKSMVVGDKTSGDYGTT
|---|
237

247 NDIAIWPENHAPLVYTYFTQPEQKAESRRDYLAAMAKIVTDS
|---|
237

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1 match found in sequence:
q9rlm4 : Beta-lactamase CTX-M-8 precursor.
(from "lactxs_spt.pep")
TOIG of: q9rlm4 check: 7690 from: 1 to: 291

ID 09RLM4 PRELIMINARY; PRT; 291 AA.
AC 09RLM4;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Beta-lactamase CTX-M-8 precursor.
GN BLACTX-M-8.
OS Citrobacter amalonaticus.
OS Plasmid pRio-2.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

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OC Citrobacter.
OX NCBI_TaxID=35703;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIO-2;
RX MEDLINE=20316814; PubMed=10858358;
RA Bonnet R., Sampaio J.L.M., Labia R., De Champs C., Siro D.,
RA Chanal C., Siro J.;
RT "A novel CTX-M beta-lactamase (CTX-M-8) in cefotaxime-resistant
RT Enterobacteriaceae isolated in Brazil."
RT Antimicrob. Agents Chemother. 44:1936-1942(2000).
DR EMBL: AF189721; AAF04388.1; -
DR HSSP: Q47066; 1BZA.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase_1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid; Signal.
FT STGNAL 1 28 POTENTIAL.
FT CHAIN 29 291 BETA-LACTAMASE CTX-M-8.
SQ SEQUENCE 291 AA; 31216 MW; 7764D1E739574C6F CRC64;

09RLM4 Length: 291 March 17, 2003 12:33 Type: P Check: 7690
Found using 'KTXS' (swope073.key)

187 LAMAQTLNLTGKALAEQRAQLVTLKGNLTGASIQGLPTSMVVGDKTSGDYGTT
|---|
237

247 NDIAIWPENHAPLVYTYFTQPEQKAESRRDYLAAMAKIVTDS
|---|
237

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1 match found in sequence:
q9s4k4 : Transposase.
(from "lactxs_spt.pep")
TOIG of: q9s4k4 check: 7119 from: 1 to: 416

ID 09S4K4 PRELIMINARY; PRT; 416 AA.
AC 09S4K4;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Transposase.
GN TNPA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JES;
RX MEDLINE=99356731; PubMed=10427724;
RA Naas T., Poirol L., Karim A., Nordmann P.;
RT "Molecular characterization of In50, a class 1 integron encoding the
RT gene for the extended-spectrum beta-lactamase VEB-1 in Pseudomonas
RT aeruginosa."
RL FEMS Microbiol. Lett. 176:411-419(1999).
DR EMBL: AF133697; AAD38926.1; -
DR InterPro: IPR002559; Transposase_11.
DR Pfam: PF01609; Transposase_11; 1.
SQ SEQUENCE 416 AA; 47719 MW; 0C62BFF5B91C6B3 CRC64;

09S4K4 Length: 416 March 17, 2003 12:33 Type: P Check: 7119
Found using 'KTXS' (swope073.key)

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219          DLANGOAKSLGCKTITKTNPINCHILITXRSKPKGTNRSTRTNCHHPSAKTYSRAKEP
          269
279          WVLASNLPPESRSPKQVNLVAKRMQIBETFRDLKSPAYGFGLR
          ...
1 match found in sequence:
q9s6r4 ; Beta-lactamase (EC 3.5.2.6).
(from "lacks_spt.pep")
TOIG of: q9s6r4 check: 345 from: 1 to: 381

ID  Q9S6R4      PRELIMINARY;      PRT;      381 AA.
AC  Q9S6R4;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE  Beta-lactamase (EC 3.5.2.6).
GN  CMY-7.
OS  Escherichia coli.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Escherichia.
OX  NCBI_TaxID=562;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CMC 27;
RT  Child J.A., Lal M., Livermore D.M., Gill M.J.;
RT  "three class C plasmid-mediated beta-lactamases from clinical isolates
RL  of E. coli from Punjab, India."
RL  Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL: A0111291; CAB36900.1;
DR  HSSP: P00811; IC3B.
DR  InterPro: IPR001466; Beta_lactamase.
DR  InterPro: IPR001586; Beta_lactamase_C.
DR  Pfam: PF00144; beta-lactamase; 1.
DR  PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW  Hydrolase.
SQ  SEQUENCE 381 AA; 42061 MW; 8BSF5AF82C707FC5 CRC64;

Q9S6R4 Length: 381 March 17, 2003 12:33 Type: P Check: 345 ..
Found using 'KTXS' (swope073.key)

...

285          MYOGLGEMILNWLKADSIINGSDSKVLAALPAVEVNPAPAVKASVHKGTSTGFGS
          335
345          YVAFVPEKNLGIYVLANKSYNPVVEAWRILEKIQ
          1---1
1 match found in sequence:
q9s6r5 ; Beta-lactamase (EC 3.5.2.6).
(from "lacks_spt.pep")
TOIG of: q9s6r5 check: 9759 from: 1 to: 381

ID  Q9S6R5      PRELIMINARY;      PRT;      381 AA.
AC  Q9S6R5;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE  Beta-lactamase (EC 3.5.2.6).
GN  CMY-6.
OS  Escherichia coli.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Escherichia.
OX  NCBI_TaxID=562;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CMC 37-16;
RT  Child J.A., Lal M., Livermore D.M., Gill M.J.;
RT  "three class C plasmid-mediated beta-lactamases from clinical isolates
RL  of E. coli from Punjab, India."
RL  Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL: A0111291; CAB36900.1;
DR  HSSP: P00811; IC3B.
DR  InterPro: IPR001466; Beta_lactamase.
DR  InterPro: IPR001586; Beta_lactamase_C.
DR  Pfam: PF00144; beta-lactamase; 1.
DR  PROSITE: PS00336; BETA_LACTAMASE_C; 1.
KW  Hydrolase.
SQ  SEQUENCE 381 AA; 41930 MW; F38E14AD038FD605 CRC64;

Q9S6R5 Length: 381 March 17, 2003 12:33 Type: P Check: 9759 ..
Found using 'KTXS' (swope073.key)

...

285          MYOGLGEMILNWLKADSIINGSDSKVLAALPAVEVNPAPAVKASVHKGTSTGFGS
          335
345          YVAFVPEKNLGIYVLANKSYNPVVEAWRILEKIQ
          1---1
1 match found in sequence:
q9suy6 ; Hypothetical 43.8 kDa protein.
(from "lacks_spt.pep")
TOIG of: q9suy6 check: 4668 from: 1 to: 398

ID  Q9SUY6      PRELIMINARY;      PRT;      398 AA.
AC  Q9SUY6;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE  Hypothetical 43.8 kDa protein.
GN  F4F15.300.
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX  NCBI_TaxID=3702;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  Alcazar J.P., Clabault G., Cottet A., Mache R., Mewes H.W., Lemcke K.,
RT  Mayer K.F.X., Quetier F., Salanoubat M.;
RT  Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RL  Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  EU Arabidopsis sequencing project;
RL  Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC  -1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
DR  EMBL: AL049711; CAB41339.1;
DR  InterPro: IPR000871; Beta_lactamase_A.
DR  InterPro: IPR001680; WD40.
DR  Pfam: PF00400; WD40; 4.
DR  SMART: SM00320; WD40; 3.
DR  PROSITE: PS00146; BETA_LACTAMASE_A; 1.
DR  PROSITE: PS50082; WD_REPEATS_2; 1.
DR  PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW  Hypothetical protein; Repeat; WD repeat.
SQ  SEQUENCE 398 AA; 43767 MW; 687F04E0EA90728 CRC64;

Q9SUY6 Length: 398 March 17, 2003 12:33 Type: P Check: 4668 ..
Found using 'KTXS' (swope073.key)

...

205          GSDNIELCRFSKDGTKPFLCAQRGDTPVWVNYDISTWKKLGFKLSKRTASTAVSL
          255
265          DGYIALGKGDGVAVAEVKTMEIYHYSKRLHLGSIASLEFCP
          255

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1 match found in sequence:
q9v076 : Hypothetical protein PAB1751.
(from "lactxs_spt.pep")
TOIG of: q9v076 check: 6496 from: 1 to: 451

ID Q9V076 PRELIMINARY; PRT; 451 AA.
AC Q9V076;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein PAB1751.
GN PAB1751.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ248285; CAB49829.1;
DR InterPro: IPR001279; Blactamase-like.
DR InterPro: IPR004613; MG423.
DR InterPro: IPR001587; UPR0036.
DR Pfam: PF00753; lactamase_B; 1.
DR Pfam: PF02147; UPR0036; 1.
DR TIGRfams: TIGR00649; MG423; 1.
DR PROSITE: PS01292; UPR0036; UNKNOWN_1.
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 451 AA; 50517 MW; AA689437804BC24E CRC64;

Q9V076 Length: 451 March 17, 2003 12:33 Type: P Check: 6496 ..
Found using 'KTXS' (swope073.key)

168 PEGAVVYACDYKFDNNHPYGERPDYKRLKELGKSGVKVLAESTRVAETTPSEAVAKM 1--1
218

228 LLEDFLYEGMEADGLIATTFASHIARLQELIEIANKMGROAIF
-----
1 match found in sequence:
q9wze7 : Dehydroase-related protein.
(from "lactxs_spt.pep")
TOIG of: q9wze7 check: 8114 from: 1 to: 269

ID Q9WZE7 PRELIMINARY; PRT; 269 AA.
AC Q9WZE7;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Dehydroase-related protein.
GN TM0681.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Uterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

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RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL: AE001740; AAD35763.1;
DR TIGR: TM0681;
DR InterPro: IPR001279; Blactamase-like.
DR InterPro: IPR000531; TonB_box.
DR Pfam: PF00753; lactamase_B; 1.
DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 269 AA; 30736 MW; 2977E1E04CA85C2 CRC64;

Q9WZE7 Length: 269 March 17, 2003 12:33 Type: P Check: 8114 ..
Found using 'KTXS' (swope073.key)

1 MPKRTTSLCRILLLENTTREGKMITNLSDRVFVIGTGTSANSVLYGKKFCVLPDS 1--1
4 7

2 matches found in sequence:
q9x4s7 : Class A beta-lactamase CFXA2.
(from "lactxs_spt.pep")
TOIG of: q9x4s7 check: 4475 from: 1 to: 321

ID Q9X4S7 PRELIMINARY; PRT; 321 AA.
AC Q9X4S7;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Class A beta-lactamase CFXA2.
GN CFXA2.
OS Prevotella intermedia.
OC Bacteria; CF group; Bacteroidetes; Bacteroidales; Prevotellaceae;
OC Prevotella.
OX NCBI_TaxID=28131;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PI 1184;
RA Mediner I., Fosse T., Labia R.;
RT "Cloning and sequence analysis of a class A beta-lactamase from
RT Prevotella intermedia.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF118110; AAD23513.1;
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 321 AA; 35376 MW; 6AD3A50316F0BDFA CRC64;

Q9X4S7 Length: 321 March 17, 2003 12:33 Type: P Check: 4475 ..
Found using 'KTXS' (swope073.key)

68 RDTVKVNNKSVYPMMSVFVKHQAALCNDFDNKGISLDTVLVINIRDKLPKTMSPYLKDY 1--1
118

128 SGPVLSITVRDLRLRYTLTOSDNNAISLMKRDVNVNAQTDSFIAT
....
204 AAMLMNRLFTFGLIDDEKOSFTIKNTLKECKTGVDRIAPLIDKEGVYLAHKRGSGYVEN 1--1
254

264 GVLAHNDVAYICLPNNISYTLAVFYKDFKNGESQASQYVAHIS

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1 match found in sequence:

q9x5a7 : Chromosomal class A beta-lactamase.
(from "lactxs_spt.pep")

TOIG of: q9x5a7 check: 6335 from: 1 to: 304

Found using 'KTXS' (swope073.key)

ID Q9X5A7 PRELIMINARY; PRT; 304 AA.
AC Q9X5A7;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Chromosomal class A beta-lactamase.
GN I2CAMP.
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Stenotrophomonas.
ON NCBI_TaxID=40324;
RX [1]
RP SEQUENCE FROM N.A.
RA Fosse T., Carles D., Giraud C., Labia R.;
RT "Cloning and sequence analysis of a new I2 type beta-lactamase
RT (I2camp) isolated from Stenotrophomonas maltophilia.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF123246; AAD37116.1; -.
DR HSSP; P00810; ITEM.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 304 AA; 31837 MW; F8D2725278DCD2 CRC64;

Q9X5A7 Length: 304 March 17, 2003 12:33 Type: P Check: 6335
Found using 'KTXS' (swope073.key)

198 AAMASLARRAVNGIOPASRQFTDMLIDNQTGACLRAGLRKMRVGDKTSGNSDDTR
248

258 NDIAVLMPHAGAVWVYTAIVLGASVDDDRRAAVLARVGTLADA

1 match found in sequence:

q9x5c0 : Beta-lactamase.
(from "lactxs_spt.pep")

TOIG of: q9x5c0 check: 5225 from: 1 to: 377

Found using 'KTXS' (swope073.key)

ID Q9X5C0 PRELIMINARY; PRT; 377 AA.
AC Q9X5C0;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Beta-lactamase.
GN AMPC.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
ON NCBI_TaxID=562;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=EI42;
RC Kim J., Kwon Y.;
RT "Characterization of AmpC type b-lactamases in clinical isolates of
RT cefoxitin-resistant Escherichia coli and Klebsiella pneumoniae.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF124201; AAD28041.1; -.

DR HSSP; P00811; ICB.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR001586; Beta_lactamase_C.
DR Pfam; PF00144; beta-lactamase; 1.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
SQ SEQUENCE 377 AA; 41500 MW; 6F1EF0A24C1275A7 CRC64;

Q9X5C0 Length: 377 March 17, 2003 12:33 Type: P Check: 5225
Found using 'KTXS' (swope073.key)

281 MYGGLGWMELMDPVNPDSIINGSGNKIYLAHPYKAITPTPAVRASWVHKGTSGFGS
331

341 YVAFIPEKEIGIVMLANKNYPNPARVAAMQIINALQ

1 match found in sequence:

q9x6w1 : Class A beta-lactamase precursor TLA-1 (EC 3.5.2.6).
(from "lactxs_spt.pep")

TOIG of: q9x6w1 check: 951 from: 1 to: 314

ID Q9X6W1 PRELIMINARY; PRT; 314 AA.
AC Q9X6W1;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Class A beta-lactamase precursor TLA-1 (EC 3.5.2.6).
GN TLA-1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
ON NCBI_TaxID=562;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20187162; PubMed=10722503;
RX Silva J., Aguilar C., Ayala G., Estrada M.A., Garza-Ramos U.,
RA Lara-Lemus R., Ledezma L.;
RT "TLA-1: a new plasmid-mediated extended-spectrum beta-lactamase from
RT Escherichia coli.";
RL Antimicrob. Agents Chemother. 44:997-1003(2000).
DR EMBL; AF148067; AAD37403.1; -.
DR HSSP; P00807; IBLP.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolyase; plasmid.
SQ SEQUENCE 314 AA; 34980 MW; 1EF7B53E011D7A53 CRC64;

Q9X6W1 Length: 314 March 17, 2003 12:33 Type: P Check: 951
Found using 'KTXS' (swope073.key)

199 DATVQLKKFKYKNELSKNSDYDLNTMIETTTGPKRLKGLLPDGTVAHKKTGSSDITNDK
249

259 GITAAITNDIGITLPLNGKHFAIAYVSDSEKSDYNEKIIEIC

1 match found in sequence:

q9x757 : Beta-lactamase.
(from "lactxs_spt.pep")

TOIG of: q9x757 check: 8563 from: 1 to: 381

ID Q9X757 PRELIMINARY; PRT; 381 AA.
 AC Q9X757;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE beta-lactamase.
 GN MIR-1.
 OS Klebsiella pneumoniae.
 OC Plasmid pmg230.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91158299; PubMed=1963529;
 RA Papanicolaou G.A., Medeiros A.A., Jacoby G.A.;
 RT "Novel plasmid mediated beta-lactamase (MIR-1) conferring resistance
 to oxytetracycline and alpha-methoxy-beta-lactams in clinical isolates of
 Klebsiella pneumoniae."
 RL Antimicrob. Agents Chemother. 34:2200-2209(1990).
 [2]
 RP SEQUENCE FROM N.A.
 RA Jacoby G.A., Tran J.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M37839; AUD2636.1; -.
 DR HSSP; P05364; 2BLT.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR001586; Beta_lactamase_C.
 DR Pfam; PF00144; beta-lactamase_1.
 DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
 DR Plasmid.
 KW SEQUENCE 381 AA; 41171 MW; DD5BID789C03142E CRC64;
 SQ

Q9X757 Length: 381 March 17, 2003 12:33 Type: P Check: 8563 ..
 Found using 'KTXS' (swope073.key)

285 MYGGLGEMLMMPVDKTVVGGSDKKVALAPLPAEVNPPAPYKASVHKGSTGGGSGS
 335

345 YVAFIPKOLGIVMLANKSYNPAFAVNAAYRILDALQ

2 matches found in sequence:

q9xb24 : AMPC beta-lactamase ACC-1 precursor (ACC-1 beta-lactamase).
 (from "lactxs_spt.pep")
 TOIG of: q9xb24 check: 9371 from: 1 to: 386

ID Q9XB24 PRELIMINARY; PRT; 386 AA.
 AC Q9XB24;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE AMPC beta-lactamase ACC-1 precursor (ACC-1 beta-lactamase).
 GN BIA-ACC-1 OR ACC-1.
 OS Klebsiella pneumoniae.
 OC Plasmid pmvp-8, and Plasmid PTNN01.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-KUS; PLASMID-PMVP-8;
 RA Baerentzen A., Schneider I., Jungwirth R., Sahly H., Ullmann U.;
 RT "A novel type of AMPC beta-lactamase, ACC-1, produced by a Klebsiella
 pneumoniae causing nosocomial pneumonia."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-KP STK54; PLASMID-PTNN01;
 MEDLINE=20291116; PubMed=10828397;
 RX

RA Nadjar D., Rouveau M., Verdet C., Donay J.L., Herrmann J.L.,
 Lagrange P.H., Philippou A., Arlet G.;
 RT "Outbreak of Klebsiella pneumoniae producing transferable Ampc-type
 beta-lactamase (ACC-1) originating from Hafnia alvei."
 RL FEMS Microbiol. Lett. 187:35-40(2000).
 DR EMBL; AJ33121; CAB46491.1; -.
 DR EMBL; AJ270942; CAB66901.1; -.
 DR HSSP; P00811; 1C3B.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR001586; Beta_lactamase_C.
 DR Pfam; PF00144; beta-lactamase_1.
 DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
 KW Plasmid; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 386
 SQ SEQUENCE 386 AA; 42057 MW; 0950C0A6894733A3 CRC64;
 Q9XB24 Length: 386 March 17, 2003 12:33 Type: P Check: 9371 ..
 Found using 'KTXS' (swope073.key)

197 EKTLLPOLGHHSTLYKVPADOMENYAWGYNKKDEPVHNMELIGNEAYGKITTSSDLRY
 247

257 VQANMGLKTDANNAKMQQALATHTHTGTFKSGEITDLMWQLEPPVSLPMLTGNMAMT

317 KSVATPIVPLPQENENWIKTGTSTNGFAYIAFVPAKKGIYMLANKNYSIDQVTVAY
 337

377 KILSLEGNK

1 match found in sequence:
 q9xb29 : Hypothetical 32.2 kDa protein (Fragment).
 (from "lactxs_spt.pep")
 TOIG of: q9xb29 check: 3032 from: 1 to: 289

ID Q9XB29 PRELIMINARY; PRT; 289 AA.
 AC Q9XB29;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE Hypothetical 32.2 kDa protein (Fragment).
 OS Klebsiella oxyloca.
 OC Plasmid pNBL63.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=571;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-NBL63;
 RX MEDLINE=99277992; PubMed=10348751;
 RA Wu S.W., Donibusch K., Kronvall G., Norgren M.;
 RT "Characterization and Nucleotide Sequence of a Klebsiella oxyloca
 cryptic Plasmid Encoding a CMY-type beta-lactamase: Confirmation that
 the Plasmid-mediated Cephamycinase Originated from the Citrobacter
 freundii AMPC beta-lactamase."
 RT Antimicrob. Agents Chemother. 43:1350-1357(1999).
 RL Antimicrob. Agents Chemother. 43:1350-1357(1999).
 DR EMBL; Y17846; CAB42616.1; -.
 KW Hypothetical protein; Plasmid.
 FT NON_TER 289 289
 SQ SEQUENCE 289 AA; 32242 MW; 58C26574D9C618C4 CRC64;

Q9XB29 Length: 289 March 17, 2003 12:33 Type: P Check: 3032 ..
 Found using 'KTXS' (swope073.key)

21 QLASEYARQNPTRKVVLDLCPQANSSSMLLGMINGENTLNGHSAIQRTKISSYIEDR
 1--1

71 74

81 IRSPYIPFNTGSSYVINWSTHNSKVNNLYLVGDEQLQLQASR

1 match found in sequence:
 q9xb3 ; Beta-lactamase CMY-5.
 (from "lactxs_spt.pep")
 TOIG of: q9xb3 check: 21 from: 1 to: 381

ID Q9XB33 PRELIMINARY; PRT; 381 AA.

AC Q9XB33;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-lactamase CMY-5.
 GN BLACW-5.
 OS Klebsiella oxytoca.
 OG Plasmid pTKH1.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Klebsiella.
 OX NCBI_TaxID=571;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KH1;
 RX MEDLINE=99277992; PubMed=10348751;
 RA Wu S.W., Dornbusch K., Kronvall G., Norgren M.;
 RT "Characterization and Nucleotide Sequence of a Klebsiella oxytoca
 RT Cryptic Plasmid Encoding a CMY-type beta-lactamase: Confirmation that
 RT the plasmid-mediated cephamycinase originated from the Citrobacter
 RT freundii Ampc beta-lactamase.";
 RL Antimicrob. Agents Chemother. 43:1350-1357(1999).
 DR EMBL; Y17716; CAB50867.1; -.
 DR HSSP; P00811; 1C3B.
 DR InterPro; IPR001466; Beta_Lactamase.
 DR InterPro; IPR001586; Beta_Lactamase_C.
 DR Pfam; PF00144; beta-lactamase: 1.
 DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
 KW Plasmid.
 SQ SEQUENCE 381 AA; 42037 MW; 889EACCE51BC43F1 CRC64;

Q9XB33 Length: 381 March 17, 2003 12:33 Type: P Check: 21 ..
 Found using 'KTXS' (swope073.key)

285 MYGIGWEMLMWPLKADSIINGSKVALALPAVEVNPAPAVKASWVHKGTGSGFGS 1--1 335

345 YVAVPEKNGIIVMLANKSPYNPVRAVRAARILEKLD

1 match found in sequence:
 q9xb7 ; Beta lactamase BlaB3.
 (from "lactxs_spt.pep")
 TOIG of: q9xb7 check: 4737 from: 1 to: 249

ID Q9XB7 PRELIMINARY; PRT; 249 AA.

AC Q9XB7;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta lactamase BlaB3.
 GN BLAB3.
 OS Flavobacterium meningosepticum.
 OC Bacteria; CFB group; Flavobacteria; Flavobacteriaceae;
 CC Chryseobacterium.
 OX NCBI_TaxID=238;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-NCRC 10016;
 RX MEDLINE=20277863; PubMed=10817691;
 RA Woodford N., Palepou M.-F.I., Babin G.S., Holmes B., Livermore D.M.;
 RT "Carbapenemases of Chryseobacterium (Flavobacterium) meningosepticum:
 RT distribution of blaB and characterization of a novel metallo-beta-
 RT lactamase gene, blaB3, in the type strain, NCRC 10016.";
 RL Antimicrob. Agents Chemother. 44:1448-1452(2000).
 DR EMBL; AF162284; AAD43582.1; -.
 DR HSSP; P04190; 2BC2.
 DR InterPro; IPR001018; Beta_Lactamase_B.
 DR InterPro; IPR001279; Lactamase-Like.
 DR Pfam; PF00753; lactamase_B; 1.
 DR Prodom; PD007656; Beta_Lactamase_B; 1.
 DR PROSITE; PS00744; BETA_LACTAMASE_B_2; 1.
 SQ SEQUENCE 249 AA; 28225 MW; F5327ED516153B5 CRC64;

Q9XB7 Length: 249 March 17, 2003 12:33 Type: P Check: 4737 ..
 Found using 'KTXS' (swope073.key)

66 VIDSPWGEERKFNFDDELYKRHKVYINNIATVSHDDRAGLEFKSLGAKTYSTKMTDS 1--1 116

126 ILAKDKPRAQYTFDNNKSFYGVKDEFGYVPGKGFADHVVVV

1 match found in sequence:
 q9xe09 ; Class A beta-lactamase SFO-1 precursor.
 (from "lactxs_spt.pep")
 TOIG of: q9xe09 check: 3849 from: 1 to: 295

ID Q9XE09 PRELIMINARY; PRT; 295 AA.

AC Q9XE09;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Class A beta-lactamase SFO-1 precursor.
 GN AMPA.
 OS Enterobacter cloacae.
 OG Plasmid pFCX300L.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99143898; PubMed=9925524;
 RA Matsumoto Y., Inoue M.;
 RT "Characterization of SFO-1, a plasmid-mediated inducible class A beta-
 RT lactamase from Enterobacter cloacae.";
 RL Antimicrob. Agents Chemother. 43:307-313(1999).
 DR EMBL; AB003148; BAA76882.1; -.
 DR HSSP; Q47066; 1BZA.
 DR InterPro; IPR001466; Beta_Lactamase.
 DR InterPro; IPR000871; Beta_Lactamase_A.
 DR Pfam; PF00144; beta-Lactamase: 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 KW Plasmid; Signal.
 FT STGNL 1 28 POTENTIAL.
 FT CHAIN 29 295 CLASS A BETA-LACTAMASE SFO-1.
 SQ SEQUENCE 295 AA; 31830 MW; 5B37B90586EB056B CRC64;

Q9XE09 Length: 295 March 17, 2003 12:33 Type: P Check: 3849 ..
 Found using 'KTXS' (swope073.key)

191 LMAKSLQTLTLCKALGEPQRAQVLEVMKNGTTGASIRAGLPATWVYGDKSGSDYGT 1--1 241

251 NDAVWPANHAPLVLYTFQPOQNAARKDVLAAAKIVTEG

1 match found in sequence:
q9zua1 ; Putative cleavage and polyadenylation specificity factor.
(from "ktxs_spt.pep")
Total of: q9zua1 check: 9997 from: 1 to: 837

ID Q9ZUA1 PRELIMINARY; PRT; 837 AA.
AC Q9ZUA1;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative cleavage and polyadenylation specificity factor.
GN ATG01730.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OK NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.T., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Bueli C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanden S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana."
RT Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006069; AAD12712.1; -;
DR InterPro: IPR001279; Blackmase-like.
DR Pfam: PF00753; lactamase B; 1.
SQ SEQUENCE 837 AA; 93119 MW; 512FD50C6A4380C4 CRC64;

Q9ZUA1 Length: 837 March 17, 2003 12:33 Type: P Check: 9997 ..
Found using 'KTXS' (swope073.key)

497 AKIVHDEISEVLHKNHVVSLACPCFKVKGESDDDDVLDIKLSAKILKTVSGAQIHE |--|
547

557 SENCLOREKEKEQFSSLLMSYSSTARDQHAPLRRHDC

-- Search Statistics --

Times: CPU Total Elapsed
00:00:01.05 00:00:15.00
Number of sequences searched: 217
Number of sequence hits: 217
Number of separate matches: 247
Number of sequence hits saved: 0

